

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1015	2adr		957	1015	6.8e-18	-0.01	0.80		ADR1; CHAIN: NULL;	ADR1, ZINC FINGER, NMR
1015	2drp	A	372	428	3.4e-06	-0.30	0.11		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1015	2drp	A	501	556	8.5e-10	-0.47	0.01		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	
1015	2gli	A	354	428	3.4e-18	-0.36	0.21		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	358	467	1.5e-26	-0.44	0.10		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	404	556	6.8e-33	-0.34	0.71		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	451	583	8.5e-33	-0.29	0.28		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	479	593	5.1e-28	-0.67	0.15		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

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										GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	2gli	A	901	1010	1e-33	-0.18	0.96		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1015	7znf		985	1013	3.4e-05	-0.23	0.31		ZINC FINGER DNA BINDING DOMAIN ZINC-FINGER (ZFY-SWAP) (NMR, 12 STRUCTURES) 7ZNF 3	
1021	2occ	A	1	299	3.4e-88	0.01	-0.17		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE FERROCYTOCHROME C: OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1023	lamu	A	48	610	0			139.53	GRAMICIDIN SYNTHETASE I; CHAIN: A, B; PHENYLALANINE; CHAIN: C, D;	PEPTIDE SYNTHETASE GRSA; PEPTIDE SYNTHETASE, GRSA, ADENYLATE FORMING
1023	llci		59	608	0			133.28	LUCIFERASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, MONOOXYGENASE, PHOTOPROTEIN, LUMINESCENCE
1028	lalh	A	98	184	3.4e-29			76.54	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1028	lmev	C	157	239	1.7e-50			97.35	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2

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1028	1hf6	A	97	269	1.4e-36			106.38	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1028	1ubd	C	130	239	6.8e-35			87.68	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN; DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1028	2gli	A	99	240	3.4e-31			87.54	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1029	1bih	A	1	351	6.8e-48			65.92	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1029	1eap	B	133	348	1.7e-10			55.72	CATALYTIC ANTIBODY 17E8 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINO)PENTYL] IEAP 3 PHOSPHONATE IEAP 4	
1029	1itb	B	54	353	1.7e-34			51.71	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE,

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1029	1kb5	-H	133	351	1.7e-08			59.81	KB5-C20 T-CELL ANTIGEN RECEPTOR; CHAIN: A, B; ANTIBODY DESIRE-1; CHAIN: L, H;	GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR) COMPLEX (IMMUNOGLOBULIN/RECEPTOR) TCR VAPHA VBETA DOMAIN: T-CELL RECEPTOR STRAND SWITCH, FAB, ANTICLONOTYPIC, 2 (IMMUNOGLOBULIN/RECEPTOR)
1029	1mam	H	139	349	1.2e-11			56.22	IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (IGG2B, KAPPA) IMAM 3	
1031	1uby		57	398	5.1e-66	-0.31	0.11		FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1031	1uby		65	397	5.1e-66			70.74	FARNESYL DIPHOSPHATE SYNTHASE; CHAIN: NULL;	TRANSFERASE FPS; TRANSFERASE, ISOPRENE BIOSYNTHESIS, CHOLESTEROL BIOSYNTHESIS
1032	1dfn	A	132	161	1.1e-12			58.55	DEFENSIN DEFENSIN /HNPS-3 IDFN 3	
1032	1dfn	A	133	161	1.1e-12	-0.35	1.00		DEFENSIN DEFENSIN /HNPS-3 IDFN 3	
1032	1dfn	A	133	161	5.1e-11	-0.35	1.00		DEFENSIN DEFENSIN /HNPS-3 IDFN 3	
1034	1a4y	A	66	224	5.7e-22	-0.15	0.35		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1034	1a9n	A	68	208	3.8e-24	0.44	0.78		U2 RNA HAIRPIN IV; CHAIN: Q;	COMPLEX (NUCLEAR

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									R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	A	93	249	1.3e-21	0.15	0.57		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	C	68	208	1.1e-23	0.52	0.80		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1a9n	C	93	249	9.5e-21	0.21	0.62		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1034	1cs6	A	279	363	3.8e-06	0.12	0.05		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1034	1cvs	C	283	364	7.6e-07	0.27	0.22		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1cvs	D	283	367	1.5e-06	0.15	0.25		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1034	1d0b	A	39	186	8.5e-19	0.22	0.74		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1034	1d0b	A	44	223	1.9e-24	0.13	0.58		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

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1034	1dce	A	106	218	1e-09	-0.25	0.03		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	ADHESION TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1dce	A	38	235	1.9e-16	0.05	-0.01		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1034	1ds9	A	104	245	1e-08	-0.76	0.10		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1034	1ds9	A	45	208	7.6e-21	-0.56	0.04		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1034	1epf	A	279	358	5.7e-07	0.10	0.98		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1034	1ev2	E	276	373	1.5e-06	0.15	0.33		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I- SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1034	1ev2	G	283	358	3.8e-06	0.12	0.77		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGFR2; FGFR2;

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									FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1034	1fo1	A	183	230	0.0013	-0.40	0.25		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1fo1	B	183	236	0.00076	-0.61	0.05		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1034	1tit		280	356	5.7e-06	0.21	0.01		TITIN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN.
1034	1tnm		279	358	1.7e-06	0.23	0.34		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	IMMUNOGLOBULIN-LIKE DOMAIN
1034	1www	X	394	490	1.7e-09	0.25	-0.19		NERVE GROWTH FACTOR; CHAIN: V, W; TRKA RECEPTOR; CHAIN: X, Y;	NERVE GROWTH FACTOR/TRKA COMPLEX BETA-NGF; COMPLEX, TRKA RECEPTOR, NERVE GROWTH FACTOR, CYSTEINE KNOT, 2
										IMMUNOGLOBULIN LIKE DOMAIN, NERVE GROWTH FACTOR/TRKA COMPLEX
1034	1yrg	A	44	198	7.6e-19	-0.34	0.24		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P, RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE- 2 RICH REPEAT PROTEIN, TWINNING,

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										HEMIEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1034	3ncm	A	279	358	9.5e-07	0.40	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN- BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1035	1cke	A	360	519	0.0019	-0.10	0.12		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1035	1coz	A	193	312	1.1e-11	0.18	0.18		GLYCEROL-3-PHOSPHATE CYTIDYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE
1035	1d6j	A	359	393	1.9e-05	-0.55	0.35		ADENOSINE- 5'PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE ADENOSINE 5' KINASE, ADENYL SULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1038	1eth	A	1	319	0			112.24	TRIACYLGLYCEROL ACYL- HYDROLASE; CHAIN: A, C; COLIPASE; CHAIN: B, D	COMPLEX (HYDROLASE/COFACTOR) TRIACYLGLYCEROL LIPASE; COMPLEX (HYDROLASE/COFACTOR), LIPID DEGRADATION
1038	1gpl		2	316	0			107.65	RP2 LIPASE; CHAIN: NULL;	SERINE ESTERASE RELATED PROTEIN 2 LIPASE; SERINE ESTERASE, HYDROLASE, LIPID DEGRADATION, PANCREAS, 2 GLYCOPROTEIN, CHIMERIC

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1038	1hpl	A	1	318	0			107.77	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL HYDROLASE) 1HPL 3	
1038	1lpb	B	1	316	0			109.40	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE AND INHIBITED ILPB 3 BY UNDECANE PHOSPHONATE METHYL ESTER (TWO CONFORMATIONS) ILPB 4	
1038	1rpl		2	316	0			100.01	PANCREATIC LIPASE RELATED PROTEIN 1; CHAIN: NULL;	HYDROLASE HYDROLASE, LIPID DEGRADATION, PANCREATIC LIPASE
1044	1ahd	P	154	219	3.4e-34	0.19	1.00		DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1AHD 3 REPLACED BY SER (C39S) COMPLEX WITH DNA (NMR, 1AHD 4 16 STRUCTURES) 1AHD 5	
1044	1au7	A	145	213	3.8e-26	-0.39	0.65		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX (DNA-BINDING PROTEIN/DNA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1044	1b72	A	158	215	1.7e-27	0.20	1.00		HOMEBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E; ULTRABITHORAX HOMEOTIC PROTEIN IV; CHAIN: A; HOMEBOX PROTEIN	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA TRANSCRIPTION/DNA ULTRABITHORAX; PBX PROTEIN; DNA BINDING, HOMEODOMAIN,
1044	1b8i	A	158	212	5.1e-29	0.33	1.00			

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									EXTRADENTICLE; CHAIN: B; DNA (5'- CHAIN: C; DNA (5'- CHAIN: D;	HOMEOTIC PROTEINS, DEVELOPMENT, 3 SPECIFICITY
1044	1fjl	A	153	213	7.6e-26	0.16	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN; DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1044	1fjl	B	155	211	1.9e-23	0.09	1.00		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN; DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1044	1ftt		155	216	1.9e-23	0.03	0.96		THYROID TRANSCRIPTION FACTOR 1 HOMEODOMAIN; IFTT 6 CHAIN: NULL; IFTT 7	DNA BINDING PROTEIN TTF-1 HD; IFTT 8 DNA BINDING PROTEIN, HOMEODOMAIN, TRANSCRIPTION FACTOR IFTT 19
1044	1ftz		153	212	5.1e-29	0.16	0.99		DNA-BINDING FUSHI TARAZU PROTEIN (HOMEODOMAIN) (NMR, 20 STRUCTURES) IFTZ 3	
1044	1nk2	P	146	223	6.8e-20			50.85	HOMEODOMAIN PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA)
1044	1nk3	P	153	215	1.9e-25	0.26	1.00		HOMEODOMAIN PROTEIN VND; CHAIN: P; DNA; CHAIN: A, B;	COMPLEX (HOMEODOMAIN/DNA) VND/NK-2 HOMEODOMAIN, VENTRAL NERVOUS SYSTEM HOMEODOMAIN, HOMEODOMAIN, DNA-BINDING PROTEIN, EMBRYONIC 2 DEVELOPMENT, COMPLEX (HOMEODOMAIN/DNA) HELIX
1044	1san		160	219	8.5e-32	0.30	0.99		DNA-BINDING PROTEIN	

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									ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 1SAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	
1046	1a4y	A	41	214	0.0095	0.27	0.46		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1048	1cke	A	6	187	6.8e-22	-0.08	0.40		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK, MSSA; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1048	1d6j	A	3	187	3.4e-23	0.08	0.33		ADENOSINE-5'PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE APS KINASE; APS KINASE, ADENYL SULFATE KINASE, SULFATE, NUCLEOTIDE 2 KINASE, TRANSFERASE
1048	1qf9	A	3	185	1.7e-21	0.34	0.99		URIDYL MONOPHOSPHATE/CYTIDYL MONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1048	1shk	A	1	186	1.7e-20	-0.06	0.84		SHIKIMATE KINASE; CHAIN: A, B;	TRANSFERASE SHIKIMATE KINASE, PHOSPHORYL TRANSFER, ADP, SHIKIMATE 2 PATHWAY, P-LOOP PROTEIN, TRANSFERASE
1048	1ukz		6	185	1.4e-19	0.35	0.64		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									COMPLEXED WITH ADP AND AMP 1UKZ 3	
1048	2cmk	A	6	187	1.7e-21	0.01	0.12		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE
1048	3adk		3	184	8.5e-22	-0.02	0.22		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	
1049	1axi	B	162	349	1.7e-10	0.18	0.48		GROWTH HORMONE; CHAIN: A; GROWTH HORMONE RECEPTOR; CHAIN: B;	COMPLEX (HORMONE/RECEPTOR) HGH; HGHBP; COMPLEX (HORMONE/RECEPTOR)
1049	1bih	A	2	338	6.8e-21	0.21	-0.14		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1049	1bj8		253	350	1.9e-14	0.35	0.42		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1bj8		360	461	3.8e-09	0.07	0.33		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1bj8		477	568	8.5e-12	0.27	0.01		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1049	1bj8		573	674	5.7e-19	0.25	0.35		GP130; CHAIN: NULL;	RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1bp3	B	158	354	1.2e-21	0.14	0.05		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	GLYCOPROTEIN
1049	1bpv		159	259	3.8e-15	0.12	0.77		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		257	351	3.8e-12	0.59	0.30		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		479	572	5.1e-11	-0.02	0.25		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		479	578	9.5e-14	0.09	0.15		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bpv		577	675	3.8e-17	0.28	0.55		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1049	1bqu	A	158	363	8.5e-19	0.02	-0.09		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	159	347	1.9e-20	-0.07	0.21		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	256	479	3.8e-12	0.25	0.03		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1bqu	A	358	581	1.7e-14	-0.05	0.10		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1bqu	A	479	681	6.8e-23	0.04	0.09		GP130; CHAIN: A, B;	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6 2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN
1049	1c8p	A	256	352	3.8e-13	0.36	0.35		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1c8p	A	359	457	7.6e-09	0.28	-0.12		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
1049	1cd9	B	159	356	9.5e-27	0.17	0.24		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	CYTOKINE G-CSF; G-CSF-R; CLASS1 CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cd9	B	360	564	7.6e-16	0.14	0.06		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR; CHAIN: B, D;	CYTOKINE G-CSF; G-CSF-R; CLASS1 CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL TRANSDUCTION
1049	1cfb		156	350	1.1e-34	-0.07	0.55		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1049	1cfb		255	456	1.9e-23	0.20	0.90		NEURAL ADHESION	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1049	lcfb		475	675	3.8e-31	0.17	0.42		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1049	lcfb		479	670	1e-18	0.35	0.06		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE ICFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS ICFB 4 (RESIDUES 610 - 814)) ICFB 5	
1049	lcs6	A	272	671	6.8e-23	0.00	-0.20		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	lcs6	A	2	349	1.7e-35	0.15	-0.08		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	lcs6	A	350	750	3.4e-15	0.12	-0.17		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1049	lcs6	A	67	464	6.8e-30	-0.08	0.10		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1cto		157	247	7.6e-13	-0.16	0.04		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		259	350	3.8e-13	0.12	0.09		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cto		479	585	7.6e-10	0.47	-0.09		GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1049	1cvs	C	74	250	6.8e-31	0.25	0.42		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	2	135	1.5e-15	0.02	-0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	61	153	5.7e-20	-0.01	0.19		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1cvs	D	74	250	1.7e-28	-0.03	0.51		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1049	1eer	B	474	555	1.5e-07	0.08	0.13		ERYTHROPOIETIN; CHAIN: A;	COMPLEX (CYTOKINE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ERYTHROPOIETIN RECEPTOR; CHAIN: B, C;	EPOBP; ERYTHROPOIETIN, ERYTHROPOIETIN RECEPTOR, SIGNAL 2 TRANSDUCTION, HEMATOPOIETIC CYTOKINE, CYTOKINE RECEPTOR 3 CLASS 1, COMPLEX (CYTOKINE/RECEPTOR)
1049	1epf	A	67	222	3.8e-14	0.02	0.27		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1049	1epf	A	71	234	6.8e-13	0.13	0.07		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1049	1ev2	E	74	250	1.7e-26	-0.02	0.65		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1ev2	G	74	254	3.4e-30	-0.14	0.12		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1evt	C	64	213	5.7e-20	-0.08	0.58		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1evt	C	74	250	1.7e-26	0.05	0.63		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									C, D;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1049	1f6f	B	160	354	3.4e-24	0.28	0.51		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1f6f	B	70	253	1.7e-16	-0.23	0.03		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1f6f	C	192	352	7.6e-10	-0.11	0.71		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1049	1fng	A	475	572	5.1e-08	0.18	-0.20		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1049	1fna		486	565	1.7e-13	0.23	0.16		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	
1049	1fna		779	866	6.8e-09	0.38	-0.20		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 IFNA 3	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	1fnf		158	565	5.1e-36	0.25	0.98		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		159	575	5.1e-36			166.16	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		479	866	3.4e-33	0.29	0.23		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		68	459	1.7e-26	0.24	0.76		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnf		772	977	3.4e-12	0.08	-0.20		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1049	1fnh	A	272	564	1.7e-20	0.22	0.55		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	361	664	3.4e-27	0.26	0.07		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	482	751	3.4e-23	0.12	-0.07		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	580	855	8.5e-25	0.01	-0.19		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	70	333	1.4e-18	0.29	0.98		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1fnh	A	774	977	3.4e-20	0.05	-0.20		FIBRONECTIN; CHAIN: A;	HEPARIN AND INTEGRIN BINDING
1049	1mfn		157	343	1.1e-27	0.21	1.00		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2
1049	1mfn		162	343	3.4e-14	0.03	1.00		FIBRONECTIN; CHAIN: NULL;	HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		259	456	1.1e-20	-0.04	0.49		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1mfn		272	459	6.8e-11	0.13	0.45		FIBRONECTIN; CHAIN: NULL;	EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn	•	360	565	3.4e-20	0.05	0.13		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		482	665	1.9e-27	0.24	0.17		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1mfn		482	665	6.8e-25	0.20	-0.05		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1049	1nct		64	152	9.5e-23	0.16	1.00		TTIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTIN5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1049	1qg3	A	160	352	1.2e-15	0.19	0.99		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB Annotation
1049	1qg3	A	361	569	3.4e-19	0.11	0.59		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	479	677	5.1e-26			103.51	INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	481	663	5.1e-26	0.23	0.43		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qg3	A	68	248	3.4e-17	0.29	0.66		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1049	1qr4	A	360	564	6.8e-12	0.24	0.43		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	711	862	3.4e-08	0.09	-0.20		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1qr4	A	776	971	3.4e-11	0.08	-0.20		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1049	1tit		65	150	1.1e-19	0.70	0.15		TTTN, I27; CHAIN: NULL;	IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN I27, TITIN IG REPEAT 27; MUSCLE PROTEIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1049	1tnm		67	152	1.9e-22	0.39	0.84		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) ITNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) ITNM 4 ITNM 58	IMMUNOGLOBULIN-LIKE DOMAIN
1049	1ttf		776	866	1.7e-09	0.39	-0.20		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	
1049	1wit		65	152	1.9e-22	0.66	-0.09		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
1049	1wwc	A	64	163	1.1e-21	0.18	0.59		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1049	2fcb	A	60	251	9.5e-13	-0.00	0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1049	2fnb	A	154	250	1.5e-14	0.55	0.68		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	2fnb	A	255	345	9.5e-14	0.76	0.16		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	2fnb	A	359	465	9.5e-10	0.02	0.10		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	2fnb	A	475	570	1.9e-13	-0.12	0.04		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1049	2fnb	A	574	670	1.5e-16	0.10	0.28		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1049	3hhr	B	162	349	1e-10	0.16	0.13		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HR 3 (EXTRACELLULAR DOMAIN) 3HR 4	
1049	3hhr	B	162	351	3.8e-27	0.24	0.03		HORMONE/RECEPTOR HUMAN GROWTH HORMONE COMPLEXED WITH ITS RECEPTOR 3HR 3 (EXTRACELLULAR DOMAIN) 3HR 4	
1049	3ncm	A	65	154	3.8e-23	0.45	0.46		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1050	1bth	A	20	157	3.4e-29	0.09	-0.06		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1050	1cs6	A	4	158	3.4e-34	0.02	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1050	1cvs	C	3	157	3.4e-41	0.12	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN:	GROWTH FACTOR RECEPTOR ² GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1050	1cvs	D	3	157	6.8e-42	0.22	0.33		C, D; FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1050	1epf	A	2	143	6.8e-22	-0.00	0.64		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1050	1ev2	E	3	157	1.7e-36	0.08	0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1ev2	E	90	162	8.5e-14	0.21	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR EGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1evt	C	3	157	1e-41	0.08	0.54		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1050	1f2q	A	2	162	1.7e-23	0.19	0.54		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1050	1feg	A	2	159	8.5e-24	-0.02	0.90		FC RECEPTOR	IMMUNE SYSTEM; MEMBRANE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FC(GAMMA)R1A; CHAIN: A;	PROTEIN CD32; FC RECEPTOR, IMMUNOGLOBULIN, LEUKOCYTE, CD32
1050	1fhg	A	1	75	1.2e-12	-0.10	0.63		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1050	1fhg	A	76	157	3.4e-17	0.37	-0.14		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1050	1fhl	A	2	147	1.9e-20	0.00	0.31		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1050	1nct		2	75	1.2e-12	0.07	0.87		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3
1050	1nct		80	158	1.7e-16	0.20	-0.09		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3
1050	1tnm		2	75	1.2e-12	0.43	0.54		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	MUSCLE PROTEIN
1050	1tnm		80	158	1.7e-16	0.07	-0.12		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1050	2dli	A	2	146	1.9e-19	-0.26	0.09		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1050	2feb	A	2	160	6.8e-25	0.14	0.69		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1051	1aln	A	26	115	3.4e-43	-0.16	0.30		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1051	1agd	A	26	115	3.4e-43	0.06	0.25		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1051	1duz	A	26	115	1.7e-42	0.18	0.22		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1051	1efx	A	26	115	5.1e-43	0.24	0.28		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1051	1hoc	A	26	116	1.4e-42	0.34	0.69		HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I	

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING IHOC 3 OF H-2D=B=, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE IHOC 4	
1051	1hsb	A	26	115	8.5e-44	0.08	0.40		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1051	1mhe	A	26	115	8.5e-43	0.13	0.25		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1051	1osz	A	26	115	1.2e-43	0.13	0.37		MHC CLASS I H-2KB HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; VESICULAR STOMATITIS VIRUS NUCLEOPROTEIN; CHAIN: C;	COMPLEX (MHC I/PEPTIDE) VSV-8; MHC/PEPTIDE COMPLEX, TRANSMEMBRANE PROTEIN, THYMIC 2 SELECTION, COMPLEX (MHC I/PEPTIDE)
1051	1qo3	A	26	115	3.4e-42	0.10	0.39		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1051	1tmc	A	26	115	8.5e-44	0.43	0.52		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	LY-49
1068	1mey	C	568	650	3.4e-49			100.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1068	1tf6	A	596	762	8.5e-38			108.39	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1068	2gli	A	327	466	3.4e-34			89.55	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI1; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1070	1a25	A	160	291	5.1e-37			68.22	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++-PHOSPHOLIPID BINDING PROTEIN; 2 CALCIUM-BINDING PROTEIN
1070	1rsy		154	283	3.4e-44			97.42	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									DOMAIN (CALB) IRSY 3	
1075	1got	B	1	322	5.1e-89			116.65	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1078	1got	B	3	345	5.1e-81			104.69	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1084	1mey	C	330	412	1.4e-48			107.26	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN; INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1084	1hf6	A	750	913	1e-37			114.17	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1084	2gli	A	302	441	1.4e-33			103.60	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1090	1evh	A	9	122	3.4e-50			82.80	MENA EVH1 DOMAIN; CHAIN: A; PEPTIDE ACTA; CHAIN: B;	CONTRACTILE PROTEIN WHI DOMAIN; MOLECULAR RECOGNITION, ACTIN DYNAMICS, CONTRACTILE PROTEIN
1090	1qc6	A	9	121	1.7e-44			62.71	EVH1 DOMAIN FROM ENA/VASP-LIKE PROTEIN; CHAIN: A, B; PHE-GLU-PHE-PRO-PRO-PRO-THR-ASP-GLU-GLU; CHAIN: C, D;	CELL MOTILITY AN INCOMPLETE SEVEN STRANDED ANTI-PARALLEL BETA BARREL 2 CLOSED BY AN ALPHA HELIX, EVH1 DOMAIN, ACTIN-BASED CELL 3 MOTILITY, INTERACTION MODULE
1095	1alh	A	391	473	1.7e-26			84.85	QCSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1095	1mey	C	418	500	1.4e-45			110.38	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1095	1tf6	A	362	530	3.4e-34			120.65	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1095	1ubd	C	336	444	3.4e-33			98.51	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1095	2gli	A	334	473	6.8e-34			105.76	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1101	1edh	A	62	266	5.1e-48			122.19	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1101	1ncj	A	61	265	6.8e-50			122.52	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1105	1aj4		72	237	8.5e-36			73.76	TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1105	1au1	B	74	249	1.7e-39			92.24	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1105	1bjf	A	65	245	1.7e-49			184.52	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING CALCIUM-BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR
1105	1cdm	A	82	234	1.4e-55			57.84	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3	
1105	1c1l		82	235	3.4e-60			67.88	CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
									CALCIUM-BINDING PROTEIN	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1105	liku		62	245	3.4e-39			160.57	CALMODULIN (VERTEBRATE) ICLL 3	
1105	lrec		68	250	1.7e-34			143.82	RECOVERIN; CHAIN: NULL; CALCIUM-BINDING PROTEIN RECOVERIN (CALCIUM SENSOR IN VISION) IREC 3	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCIUM-BINDING PROTEIN
1105	ltcf		70	235	1.5e-39			73.38	TROPONIN C; CHAIN: NULL; CONTRACTILE SYSTEM	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION
1105	ltmx		67	233	1e-38			69.96	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CALCIUM-BINDING PROTEIN EF- HAND ITNX 14
1105	ltop		63	237	8.5e-40			73.36	PROTEIN TROPONIN C ITOP 3	
1105	lvrk	A	79	236	3.4e-59			68.28	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1105	2sep	A	34	205	3.4e-09			53.97	BINDING PROTEIN SARCOPLASMIC CALCIUM- BINDING PROTEIN 2SCP 3	
1114	lam4	D	51	216	6.8e-48			70.86	P50-RHO GAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE- ACTIVATING/GTP-BINDING) COMPLEX (GTPASE- ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1114	lbyu	A	45	231	8.5e-52			74.78	GTP-BINDING PROTEIN RAN;	TRANSPORT PROTEIN TC4; GTPASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1114	1byu	B	41	231	1.7e-52			69.65	CHAIN: A, B; GTP-BINDING PROTEIN RAN; CHAIN: A, B;	NUCLEAR TRANSPORT, TRANSPORT PROTEIN TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1114	1cly	A	50	216	1.7e-63			67.97	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1114	1ctc	A	50	217	1.7e-62			75.99	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1114	1cxz	A	47	222	1.5e-54			82.44	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1114	1hur	A	37	218	5.1e-12			71.40	HUMAN ADP-RIBOSYLATION FACTOR 1; IHUR 5 CHAIN: A, B; IHUR 7	PROTEIN TRANSPORT GDP-BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED IHUR 16
1114	1lbr	A	52	221	3.4e-51			86.05	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1114	1kao		50	217	3.4e-60			79.99	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1114	1mhl		49	222	1.2e-54			77.42	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1114	1nlp	C	47	231	3.4e-51			89.47	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1114	1x4	B	51	216	1.4e-51			70.72	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	TRANSPORT COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP- BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1114	1zbd	A	49	226	1.7e-63			93.30	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	
1114	2ngr	A	50	230	3.4e-50			77.06	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	
1114	3rab	A	47	221	6.8e-65			102.45	RAB3A; CHAIN: A;	
1116	2bnh		2	324	1.7e-52			56.47	RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE RAS-ONCOGENE INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1120	5pnt		2	140	1.4e-54			214.70	LOW MOLECULAR WEIGHT PHOSPHOTYROSYL PHOSPHATASE; CHAIN: NULL;	HYDROLASE ORTHOPHOSPHORIC MONOESTER PHOSPHOHYDROLASE; HYDROLASE, ACETYLATION, TYROSINE PHOSPHATASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1122	1av1	A	83	280	5.1e-05			51.65	APOLIPOPROTEIN A-I; CHAIN: A, B, C, D;	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDL, LCAT-ACTIVATION
1127	1e0l	A	465	741	3.4e-76			100.75	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1127	1a5i	A	454	739	5.1e-67			106.52	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	COMPLEX (SERINE PROTEASE/INHIBITOR) (DELTA FEK) DSPAALPHA I; EGRCMK; SERINE PROTEASE, FIBRINOLYTIC ENZYMES, PLASMINOGEN 2 ACTIVATORS
1127	1aht	H	465	744	1.5e-73			91.53	ALPHA-THROMBIN; 1AHT 4 CHAIN: L, H; 1AHT 5 HIRUGEN; 1AHT 8 CHAIN: I; 1AHT 9	COMPLEX (SERINE PROTEINASE/INHIBITOR)
1127	1aut	C	464	739	5.1e-68			99.33	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1127	1ekb	B	468	739	1.7e-76			89.82	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROPEPTIDASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1127	1etr	H	465	745	1.5e-71			92.09	HYDROLASE(SERINE PROTEINASE) EPSILON-THROMBIN (E.C.3.4.21.5) NON-COVALENT COMPLEX WITH IETR 3 MQPA IETR 4	
1127	1fxy	A	463	742	1.4e-76			89.40	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE , PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
1127	1kig	H	465	745	3.4e-70			98.96	FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1127	1mkx	K	425	739	1.7e-72			93.49	ALPHA-THROMBIN; CHAIN: L, H; PRETHROMBIN-2; CHAIN: K;	COMPLEX (BLOOD COAGULATION/PROENZYME) COMPLEX (BLOOD COAGULATION/PROENZYME), THROMBIN, 2 PRETHROMBIN-2, PLASMA, SERINE PROTEASE
1127	1pyt	D	454	739	1.5e-75			95.69	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TC; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE
1127	1rtf	B	467	740	1.7e-68			102.89	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
1135	1mey	C	342	430	6.8e-47			71.69	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Pst Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1135	1tf3	A	342	433	1.5e-21			67.88	TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE; CHAIN: E, F;	(ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE; NMR, TFIIIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 5S RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION REGULATION/DNA)
1135	1tf6	A	276	454	3.4e-41			105.09	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1135	1ubd	C	277	400	1.7e-30			80.44	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1135	2gli	A	277	431	1.4e-60			202.77	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1139	1mab	B	1	183	1.7e-46			64.40	F1-ATPASE ALPHA CHAIN; CHAIN: A; F1-ATPASE BETA CHAIN; CHAIN: B; F1-ATPASE GAMMA CHAIN; CHAIN: G;	HYDROLASE ATP SYNTHASE, FO F1-ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1140	lmab	B	51	264	6.8e-66			130.11	F1-ATPASE ALPHA CHAIN; CHAIN: A; F1-ATPASE BETA CHAIN; CHAIN: B; F1-ATPASE GAMMA CHAIN; CHAIN: G;	HYDROLASE ATP SYNTHASE, FOF1-ATPASE, OXIDATIVE PHOSPHORYLATION, 2 MITOCHONDRIA, HYDROLASE
1148	lcrz	A	3	122	1.6e-09	0.19	0.17		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1148	lelj	A	11	127	3.2e-29	0.70	0.94		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	lelj	A	3	79	3.2e-10	0.16	0.18		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1148	lgot	B	6	122	8e-22	0.01	0.40		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1149	lef1	A	43	326	1.4e-97	0.69	1.00		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN
1153	1a06		36	339	0			329.67	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1153	1a06		6	334	0	0.64	1.00		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1155	1cfe		51	203	1e-28			82.01	PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1155	1cfe		52	203	1e-28	0.47	1.00		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1156	1ds6	A	1	96	1.2e-46	0.06	1.00		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;	SIGNALING PROTEIN P21-RAC2; RHO GDI 2, RHO-GDI BETA, LY-GDI; BETA SANDWICH, PROTEIN- PROTEIN COMPLEX, G-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING PROTEIN
1159	1qf9	A	23	239	1.5e-19	-0.03	0.62		URIDYL MONOPHOSPHATE/CYTIDYL MONOPHOSPHATE KINASE; CHAIN: A;	KINASE UMP/CMP KINASE; NUCLEOSIDE MONOPHOSPHATE KINASE, NMP KINASE, PHOSPHORYL 2 TRANSFER, TRANSITION STATE ANALOG COMPLEX, TRANSFERASE
1159	1qhf	A	249	424	5.1e-47	0.47	1.00		PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
1159	1qhf	A	250	449	5.1e-47			63.00	PHOSPHOGLYCERATE MUTASE; CHAIN: A, B;	TRANSFERASE TRANSFERASE (PHOSPHORYL)
1159	3adk		36	236	3.4e-26	-0.17	0.68		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1159	3pgm		249	441	1.7e-48	0.19	1.00		TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	
1159	3pgm		249	441	1.7e-48			58.96	TRANSFERASE (PHOSPHORYL) PHOSPHOGLYCERATE MUTASE (E.C.2.7.5.3) DE- PHOSPHO ENZYME 3PGM 4	
1159	3trmk	A	34	237	1.2e-29	-0.13	0.19		THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	KINASE KINASE, PHOSPHOTRANSFERASE
1160	1mey	C	360	442	4.8e-51			100.83	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1160	1hf6	A	276	437	8e-38			108.88	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
1160	1ubd	C	334	442	5.1e-53			86.63	YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1160	2gli	A	304	443	3.2e-34			98.31	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										BINDING PROTEIN/DNA)
1163	1a06		43	340	3.2e-84			130.42	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1163	1a60		18	334	6.8e-54			108.45	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1163	1apm	E	18	353	0			168.88	TRANSFERASE(PHOSPHOTRANSFERASE) SC-/AMPS-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (SC/APKS) 1APM 3 (CATALYTIC SUBUNIT) ALPHA ISOENZYME MUTANT WITH SER 139 1APM 4 REPLACED BY ALA (/S139A\$) COMPLEX WITH THE PEPTIDE 1APM 5 INHIBITOR PKI(5-24) AND THE DETERGENT MEGA-8 1APM 6	
1163	1aq1		50	348	4.8e-56			111.26	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1163	1bi8	A	51	323	6.8e-56			93.00	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1163	1blx	A	47	331	6.8e-62			113.75	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									B;	PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1163	1byg	A	44	300	1.3e-31			93.49	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUFOSPORINE, TRANSFERASE
1163	1cmk	E	9	353	0			175.36	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1163	1ctp	E	15	343	0			168.10	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1163	1fgk	A	39	309	6.4e-31			106.44	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1fgk	B	36	304	1.3e-37			117.87	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1163	1hcl		50	348	1e-66			128.78	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1163	1if3	A	38	323	3.2e-26			99.07	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1163	1jak		38	388	5.1e-64			104.42	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1163	1kob	A	24	359	1e-90			159.16	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1163	1p38		31	395	1.6e-50			109.88	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1163	1phk		49	305	1.1e-83			156.26	PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1163	1pme		44	389	9.6e-46			104.21	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1163	1tki	A	47	370	8e-57			131.84	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1163	3erk		36	400	3.4e-69			116.38	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TTIN, MUSCLE, AUTOINHIBITION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1170	1bw m	A	17	247	1.6e-12			50.07	ALPHA-BETA T CELL RECEPTOR (TCR) (D10); CHAIN: A;	IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNORECEPTOR, IMMUNE SYSTEM
1170	1cdy		22	190	0.00034			50.90	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1170	1f58	H	17	244	4.8e-21			51.50	IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN(GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2, V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1170	1fig	H	17	239	8e-19			51.43	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT IFIG 3	
1170	1qtm	D	14	219	6.4e-23			50.17	MHC CLASS I HLA-A; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE P6A; CHAIN: C; HMAN T-CELL RECEPTOR; CHAIN: D; HLA-A 0201; CHAIN: E;	IMMUNE SYSTEM HUMAN TCR/PEPTIDE/MHC COMPLEX, HLA-A2, HTLV-1, TAX, TCR, T 2 CELL RECEPTOR, IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1170	2gfb	A	15	240	1.6e-17			51.08	IMMUNOGLOBULIN IGG2A FAB FRAGMENT (CNJ206) 2GFB ₃	
1170	2pcp	B	17	239	9.6e-21			51.13	IMMUNOGLOBULIN; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN
1174	1a17		152	245	0.0017	-0.20	0.04		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICHOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1180	1f1b		195	418	1.7e-53			129.15	GAMMA-FIBRINOGEN CARBOXYL TERMINAL FRAGMENT; CHAIN: NULL;	BLOOD COAGULATION FACTOR BLOOD COAGULATION, GLYCOPROTEIN, CALCIUM, PLATELET, PLASMA, 2 ALTERNATIVE SPLICING, SIGNAL, DISEASE MUTATION, POLYMORPHISM
1180	1fzc	B	148	416	1.7e-63			132.32	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fzc	C	151	422	3.4e-62			141.90	FIBRIN; CHAIN: A, B, C, D, E, F, G, H, I, J;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA PROTEIN, CROSSLINKING
1180	1fzd	A	242	419	1.7e-57			154.36	FIBRINOGEN-420; CHAIN: A, B, C, D, E, F, G, H;	BLOOD COAGULATION BLOOD COAGULATION, FIBRINOGEN-420, ALPHAEBC DOMAIN, 2 FIBRINOGEN RELATED DOMAIN, GLYCOSYLATED PROTEIN
1180	1fzg	C	170	419	1.1e-39			141.24	FIBRINOGEN; CHAIN: A, B, C, D, E, F, S, T, M, N;	BLOOD COAGULATION BLOOD COAGULATION, PLASMA, PLATELET, FIBRINOGEN, FIBRIN
1180	1fzg	E	160	416	3.2e-39			130.27	FIBRINOGEN; CHAIN: A, B, C,	BLOOD COAGULATION BLOOD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									D, E, F, S, T, M, N;	COAGULATION, PLASMA, PLATELET, FIBRINOGEN, FIBRIN
1181	1fjm		2	104	1.6e-43			145.02	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: NULL;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1gif	A	1	115	1.6e-52			180.54	GLYCOSYLATION-INHIBITING FACTOR; CHAIN: A, B, C;	CYTOKINE MACROPHAGE, INFLAMMATORY RESPONSE, CYTOKINE
1181	1mfi	A	2	115	3.2e-52			170.94	MACROPHAGE MIGRATION INHIBITORY FACTOR; CHAIN: A, B, C;	CYTOKINE PHENYLPIRUVATE TAUTOMERASE; CYTOKINE, MACROPHAGE, INFLAMMATORY RESPONSE, TAUTOMERASE
1185	1d2n	A	195	450	1.2e-35			76.43	N-ETHYLMALIMIDE-SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN, HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1195	1a8y		382	723	4.8e-25			91.59	CALSEQUESTRIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN, CALSEQUESTRIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
1200	1ayz	A	31	190	3.2e-47			71.29	UBIQUITIN-CONJUGATING ENZYME RAD6; CHAIN: A, B, C;	UBIQUITIN CONJUGATION UBC2; UBIQUITIN CONJUGATION, UBIQUITIN-CONJUGATING ENZYME
1200	1c4z	D	47	191	9.6e-40			84.49	UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2; CHAIN: D;	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
1200	1qcq	A	44	193	3.2e-53			81.61	UBIQUITIN CONJUGATING ENZYME; CHAIN: A;	LIGASE UBIQUITIN, UBIQUITIN-CONJUGATING ENZYME, YEAST

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1200	1u9a	A	24	193	1.6e-43			74.19	UBC9; CHAIN: NULL;	UBIQUITIN-CONJUGATING ENZYME UBIQUITIN-CONJUGATING ENZYME; UBIQUITIN-CONJUGATING ENZYME, UBIQUITIN-DIRECTED 2 PROTEOLYSIS, CELL CYCLE CONTROL, LIGASE
1200	2aak		31	193	3.2e-47			71.32	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC1; UBIQUITIN CONJUGATION, LIGASE
1200	2e2c		26	193	1.4e-41			67.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBIQUITIN CONJUGATION, UBIQUITIN CARRIER PROTEIN, THIOESTER 2 BOND, LIGASE
1200	2ucz		33	193	3.2e-43			64.54	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1204	1awj		241	317	3.2e-15	-0.35	0.06		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T-CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1204	1aww		250	319	1.1e-13	0.55	0.58		BRUTON'S TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE ATK, AMGX1, BPK; TYROSINE KINASE, X-LINKED AGAMMAGLOBULINEMIA, XLA, BTK, SH3 2 DOMAIN, TRANSFERASE
1204	1bul	A	258	318	4.8e-15	0.03	0.21		HEMOPOIETIC CELL KINASE; CHAIN: A, B, C, D, E, F;	TRANSFERASE TYROSINE-PROTEIN KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3
1204	1efn	A	258	317	1.6e-17	0.12	0.82		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, FXXP MOTIF
1204	1fyn	A	255	318	6.4e-19	0.32	0.58		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1204	lgr	A	260	322	4.8e-12	0.25	0.63		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL IGBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE IGBR 4 (NMR, 29 STRUCTURES) IGBR 5	
1204	lnlo	C	259	316	1.3e-16	0.42	0.69		C-SRC; CHAIN: C; NLI (MN7-MN2-MN1-PLPLP); CHAIN: N;	COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMAIN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PEPTIDE)
1204	lqly	A	257	318	4.8e-13	0.41	0.43		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTON'S TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1204	lshf	A	256	318	8e-19	0.39	0.31		PHOSPHOTRANSFERASE FYN	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1204	2ab1		251	423	9.6e-28	0.04	-0.15		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1204	4hck		255	318	3.2e-15	0.04	0.55		HEMATOPOIETIC CELL KINASE; CHAIN: NULL;	TRANSFERASE HCK; SH3, PROTEIN TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE
1205	1exy	A	38	98	0.0096	0.69	0.19		CYTOCHROME B5; CHAIN: A;	ELECTRON TRANSPORT HELIX, BETA-STRAND, ELECTRON TRANSPORT
1208	1cho	I	554	592	5.1e-07	-0.30	0.58		COMPLEX(SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY 1CHO 4 OVOMUCOID THIRD DOMAIN (OMTKY35) 1CHO 5	
1208	1ldt	L	559	587	1.7e-07	-0.23	0.86		TRYPSIN; CHAIN: T; TRYPTASE INHIBITOR; CHAIN: L;	COMPLEX (HYDROLASE/INHIBITOR) LDTI; COMPLEX (HYDROLASE/INHIBITOR), HYDROLASE, INHIBITOR, 2 INFLAMMATION, TRYPTASE
1215	1ak8		356	410	3.4e-05	-0.15	0.05		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN CERUIM TRIC- DOMAIN, RESIDUES 1 - 75; CERUIM- LOADED, CALCIUM-BINDING PROTEIN
1215	1c7w	A	349	410	6.8e-06	-0.50	0.23		CALCIUM VECTOR PROTEIN;	METAL BINDING PROTEIN CAVP;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1215	1cdm	A	356	418	3.4e-05	-0.48	0.09		CHAIN: A; CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II ICDM 4 COMPLEX(SERINE PROTEINASE-INHIBITOR) ALPHA-CHYMOTRYPSIN (E.C.3.4.21.1) COMPLEX WITH TURKEY ICHO 4 OVOMUCOID THIRD DOMAIN (OMTKY3S) ICHO 5	EF-HAND FAMILY, CALCIUM BINDING PROTEIN, NMR
1215	1cho	I	39	84	5.1e-10	0.04	0.65		CARDIAC TROPONIN C; CHAIN: A; CALMODULIN; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1215	1dl	A	349	410	1.7e-05	-0.26	0.21		THERMAL HYSTERESIS PROTEIN ISOFORM YL-1; CHAIN: A, B;	ANTIFREEZE PROTEIN INSECT
1215	1ext	A	348	414	1.4e-05	0.15	0.05			ANTIFREEZE PROTEIN, THERMAL HYSTERESIS, TENEBRIO 2 MOLITOR, IODINATION, RIGHT-HANDED BETA-HELIX, TMAPP
1215	1ezg	A	226	305	3.2e-06	0.21	0.13		CALMODULIN; CHAIN: A;	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE
1215	1f71	A	349	410	6.8e-05	0.10	0.69		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4
1215	1fak	L	236	302	4.8e-09	0.07	-0.19			

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1215	1nub	A	201	426	1.7e-28			73.86	BASMENT MEMBRANE PROTEIN BM-40; CHAIN: A, B;	PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING
1215	1qjt	A	348	419	6.8e-07	-0.05	0.01		EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE CHAIN: A;	EXTRACELLULAR MODULE OSTONECTIN, SPARC, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, GLYCOPROTEIN, ANTI-ADHESIVE PROTEIN, 2 COLLAGEN BINDING, SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES
1215	1tro		348	410	3.4e-05	-0.37	0.19		CALCIUM-BINDING PROTEIN RAT ONCOMODULIN 1RRO 3	GROWTH FACTOR EHI; EH DOMAIN, EPS15, EF-HAND, SOLUTION STRUCTURE, S100 PROTEIN
1215	1sgp	I	43	84	1.7e-08	0.67	0.55		STREPTOMYCES GRISEUS PROTEINASE B; 1SGP 6 CHAIN: E; 1SGP 7 TURKEY OVOMUCOID INHIBITOR; 1SGP 11 CHAIN: I; 1SGP 12	COMPLEX (SERINE PROTEASE/INHIBITOR) SGPB; 1SGP 8 ALA18-OMTKY3; 1SGP 14 SERINE PROTEINASE, PROTEIN INHIBITOR 1SGP 25
1215	1sra		279	423	1.5e-38	0.43	0.72		SPARC; 1SRA 4 CHAIN: NULL; 1SRA 5	CALCIUM-BINDING PROTEIN BM-40, OSTONECTIN; 1SRA 7 EXTRACELLULAR MATRIX PROTEIN 1SRA 20
1215	1sra		279	426	1.5e-38			58.51	SPARC; 1SRA 4 CHAIN: NULL; 1SRA 5	CALCIUM-BINDING PROTEIN BM-40, OSTONECTIN; 1SRA 7 EXTRACELLULAR MATRIX PROTEIN 1SRA 20
1215	1xka	L	240	313	4.8e-09	0.09	-0.19		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1215	3ovo		40	84	1.7e-09	0.76	0.21		PROTEINASE INHIBITOR (KAZAL) OVOMUCOID THIRD DOMAIN CLEAVED RDI 3OVO 3	GROWTH FACTOR LIKE DOMAIN
1215	5pal		348	410	3.4e-05	-0.11	0.13		CALCIUM-BINDING PROTEIN PARVALBUMIN (ALPHA LINEAGE) SPAL 3	
1215	9wga	A	112	286	3.2e-15	0.08	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1216	1a8a		1	217	3.2e-51	0.58	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1216	1a8a		1	217	3.2e-51			75.48	ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1216	1ain		61	222	1e-68	0.23	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ain		61	223	1e-68			170.55	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ain		62	222	4.8e-67	-0.02	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1216	1ala		1	214	3.2e-53	0.42	1.00		CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN V 1ALA 3	
1216	1ala		1	214	3.2e-53			75.25	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN V 1ALA 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1216	1ann		11	215	9.6e-51	0.42	1.00		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1ann		1	216	3.2e-67			68.51	ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1ann		62	219	3.2e-67	0.46	1.00		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1216	1avc		10	216	1.6e-50	0.24	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1216	1avc		5	221	9.6e-78	0.48	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Fsi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1216	1axn		4	216	9.6e-53	0.76	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	PROTEIN CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	1axn		53	223	3.2e-67			84.90	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	1axn		59	222	3.2e-67	0.70	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1216	1hvd		1	212	1.1e-49			69.28	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL 1HVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION 1HVD 4 WITH GLU 17 REPLACED BY GLY (E17G) 1HVD 5	
1217	1a8a		8	189	8e-39	0.64	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1217	1ain		13	187	8e-32	0.22	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1217	1ain		33	304	0			403.43	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1217	1ain		35	300	0	0.17	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I 1AIN 3	
1217	1ala		8	186	3.2e-38	0.31	1.00		CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN V 1ALA 3	

SEQ ID NO:	PDB ID	CHAI NID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1217	1ann		8	187	3.2e-38	0.55	1.00		ANNEXIN IV; 1ANN 5 CHAIN: NULL; 1ANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; 1ANN 7-12 5KB CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1217	1avc		8	186	4.8e-26	0.28	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN II, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1217	1axn		8	187	1.6e-37	0.54	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1217	1hvd		8	184	6.4e-38	0.31	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	
1218	1a8a		31	195	3.2e-66			58.84	ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1a8a		33	194	3.2e-66	0.68	1.00		ANNEXIN V; CHAIN: NULL;	PHOSPHOLIPID ANALOG PLACENTAL ANTICOAGULANT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										PROTEIN; PHOSPHOLIPID ANALOG, CALCIUM BINDING PROTEIN, MEMBRANE 2 BINDING PROTEIN
1218	1ain		33	194	1e-68	0.23	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ain		33	195	1e-68			170.39	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ain		35	194	1.6e-65	0.15	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN I IAIN 3	
1218	1ann		33	195	3.2e-68			65.05	ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; IANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1ann		34	190	3.2e-68	0.54	1.00		ANNEXIN IV; IANN 5 CHAIN: NULL; IANN 6	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN 32.5 KD CALECTRIN, ENDONEXIN I; IANN 7 32.5KD CALECTRIN, ENDONEXIN I, LIPOCORTIN IV, IANN 12 2 CHROMOBINDIN IV, PROTEIN II IANN 13
1218	1avc		2	186	1.6e-38	0.30	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING, MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1avc		34	193	1.6e-71	0.61	1.00		ANNEXIN VI; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN P68, PROTEIN III, 67-KDA-CALCIMEDIN, LIPOCORTIN ANNEXIN, CALCIUM-BINDING,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1218	1axn		25	195	6.4e-67			85.90	ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	MEMBRANE-BINDING, 2 CALCIUM/PHOSPHOLIPID-BINDING PROTEIN
1218	1axn		31	194	6.4e-67	0.70	1.00		ANNEXIN III; 1AXN 4 CHAIN: NULL; 1AXN 5	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1218	1dk5	A	2	169	3.2e-19	0.02	1.00		ANNEXIN 24(CA32); CHAIN: A, B;	CALCIUM/PHOSPHOLIPID-BINDING PROTEIN ANNEXIN FAMILY 1AXN 14
1218	1hvd		32	195	9.6e-68			68.02	CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	METAL BINDING PROTEIN PLANT ANNEXIN, CAPSICUM ANNUUM, BELL PEPPER, CALCIUM 2 BINDING PROTEIN
1218	1hvd		33	194	9.6e-68	0.59	1.00		CALCIUM/PHOSPHOLIPID BINDING ANNEXIN V (LIPOCORTIN V, ENDONEXIN II, PLACENTAL IHVD 3 ANTICOAGULANT PROTEIN) (CALCIUM IONS ARE VISIBLE) MUTATION IHVD 4 WITH GLU 17 REPLACED BY GLY (E17G) IHVD 5	
1219	1b3u	A	23	627	1.6e-45			120.56	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1219	1b3u	A	320	643	1.6e-09	0.07	0.23		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHORYLATION, HEAT REPEAT SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1219	1b3u	A	71	625	1.6e-45	0.04	-0.07		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1219	1ee4	A	211	473	1.7e-10	0.36	1.00		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1ee4	A	279	643	1.4e-44	0.57	0.86		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1219	1ial	A	179	628	1.3e-43			118.96	IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1ial	A	272	643	1.3e-43	0.50	0.53		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1219	1ibr	B	318	633	4.8e-15	0.01	-0.15		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1219	2bet		239	643	1.1e-39	0.51	0.06		BETA-CATENIN; CHAIN: NULL;	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1219	3bct		277	643	3.2e-35	0.46	0.24		BETA-CATENIN; CHAIN: NULL;	CATENIN, STRUCTURAL PROTEIN
										ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1221	1bu7	A	19	486	9.6e-53			174.17	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1221	1oxa		27	486	3.2e-24			94.76	CYTOCHROME P450 ERYF; IOXA 5 CHAIN: NULL IOXA 6	OXIDOREDUCTASE (OXYGENASE)
1222	1bu7	A	35	324	1.3e-18	-0.20	0.04		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1bu7	A	61	318	3.4e-36	-0.23	0.29		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1222	1dt6	A	31	325	3.2e-92	-0.02	0.99		CYTOCHROME P450 2C5; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYP11C5 P450 1, MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(a) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
1222	1f26	A	48	318	1.7e-21	-0.08	0.05		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
1222	1oxa		61	318	6.8e-33	-0.40	0.28		CYTOCHROME P450 ERYF; IOXA 5 CHAIN: NULL IOXA 6	OXIDOREDUCTASE (OXYGENASE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1227	1crz	A	130	352	0.00032	-0.06	0.04		TOLB PROTEIN; CHAIN: A;	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD
1227	1erj	A	116	431	4.8e-73	0.57	1.00		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1erj	A	4	285	1.3e-58	0.40	0.29		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1erj	A	65	373	1.6e-66	0.38	1.00		TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	TRANSCRIPTION INHIBITOR BETA-PROPELLER
1227	1got	B	12	370	1.3e-77			119.11	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1227	1got	B	14	328	1.3e-77	0.14	0.53		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1227	1got	B	166	431	4.8e-54	0.64	1.00		GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1235	1aif	H	413	518	0.0068	-0.14	0.35		ANTI-IDIOTYPIC FAB 409.53 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN
1235	1qun	B	321	580	1.2e-15	-0.00	-0.18		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1235	1qun	B	408	701	6.8e-16	0.11	-0.19		PAPD-LIKE CHAPERONE FIMC; CHAIN: A, C, E, G, I, K, M, O; MANNOSE-SPECIFIC ADHESIN FIMH; CHAIN: B, D, F, H, J, L, N, P;	CHAPERONE/STRUCTURAL PROTEIN CHAPERONE ADHESIN DONOR STRAND COMPLEMENTATION, 2 CHAPERONE/STRUCTURAL PROTEIN
1236	1fs2	A	214	293	0.00034	-0.25	0.13		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2- ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1236	1pjr		430	960	3.2e-68	-0.22	0.58		PCRA; CHAIN: NULL;	HELICASE DNA REPAIR, DNA REPLICATION, SOS RESPONSE, HELICASE, 2 ATP-BINDING, DNA-BINDING
1236	1uaa	A	441	872	1.6e-47	-0.55	0.00		ATP-DEPENDENT DNA HELICASE REP; CHAIN: A, B; DNA CHAIN: C;	COMPLEX (HELICASE/DNA) COMPLEX (HELICASE/DNA), HELICASE, DNA UNWINDING
1236	2pjr	A	436	991	1.3e-62			90.62	HELICASE PCRA; CHAIN: A, F;	HYDROLASE/DNA ATP-DEPENDENT

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQOL D score	Compound	PDB annotation
									HELICASE PCRA; CHAIN: B, G; DNA (5'-D(*TP*TP*TP*TP*J-3'); CHAIN: C, D; DNA (5'-D(*GP*C)-3'); CHAIN: H; DNA (5'-D(*AP*CP*TP*GP*C)-3'); CHAIN: I;	HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX
1237	1e4y	A	10	213	3.4e-22	-0.01	0.89		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a4y	A	126	299	6.4e-07	0.04	0.09		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPIPOPE MAPPING, LEUCINE-RICH 3 REPEATS
1237	1a9n	A	12	151	3.4e-13	0.04	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRP,RIBONUCLEOPROTEIN
1237	1a9n	A	20	101	3.2e-07	0.28	0.51		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRP,RIBONUCLEOPROTEIN
1237	1a9n	A	51	187	8.5e-24	0.36	0.71		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRP,RIBONUCLEOPROTEIN
1237	1a9n	A	72	196	3.4e-20	0.04	0.04		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRP,RIBONUCLEOPROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1237	1a9n	C	20	101	3.2e-07	0.49	0.35		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	SNRNP, RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1a9n	C	51	192	5.1e-24	0.05	0.66		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1237	1d0b	A	3	187	3.2e-25	-0.14	0.71		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	44	221	6.8e-29	-0.20	0.07		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1d0b	A	75	268	6.4e-21	0.15	-0.02		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1237	1dce	A	11	100	1.6e-11	0.35	0.96		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	130	233	3.2e-13	0.47	0.94		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	160	278	4.8e-10	0.20	-0.03		RAB GERANYLGERANYLTRANSFERASE	TRANSFERASE CRYSTAL STRUCTURE, RAB

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1dce	A	44	169	3.2e-11	0.21	0.33		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N- FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1237	1ds9	A	11	146	4.8e-12	-0.31	0.09		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1ds9	A	130	252	3.2e-14	-0.20	0.22		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1ds9	A	37	169	1.6e-11	-0.54	0.45		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1237	1fo1	A	132	192	1.1e-06	-0.03	0.65		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)
1237	1fo1	B	132	192	1.1e-06	0.25	0.60		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP, RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)
1237	1fs2	A	10	206	1.2e-25	0.15	0.46		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2- ASSOCIATED P45; CYCLIN A/CDK2-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1237	1fs2	A	130	294	1.1e-06	0.34	0.22		SKP2; CHAIN: A, C, SKP1; CHAIN: B, D;	ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1237	2bnh		19	223	1.5e-28	-0.03	0.82		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1238	1a17		119	279	1e-18	0.10	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1238	1a17		133	250	6.4e-14	0.27	0.51		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		153	296	4.8e-13	0.30	0.76		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		20	153	8e-13	0.01	0.23		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1238	1a17		221	368	5.1e-19	0.31	0.99		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		232	348	9.6e-13	0.56	0.94		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		263	392	9.6e-13	0.22	0.80		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		290	416	3.2e-14	0.22	0.52		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		29	142	1.7e-15	0.18	0.11		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		300	414	1.7e-18	-0.14	0.74		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY
1238	1a17		338	421	4.8e-13	0.41	0.37		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	STRUCTURE HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1a17		56	184	1.7e-15	0.18	0.70		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		63	175	8e-10	0.34	0.41		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		85	209	4.8e-11	0.12	0.58		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1a17		89	212	3.4e-17	0.12	0.65		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1238	1d8d	A	217	410	4.8e-07	-0.23	0.60		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER
1238	1d8d	A	28	266	3.4e-15	-0.04	0.18		FARNESYLTRANSFERASE (ALPHA SUBUNIT); CHAIN: A; FARNESYLTRANSFERASE (BETA SUBUNIT); CHAIN: B; K-RAS4B PEPTIDE SUBSTRATE; CHAIN: P;	TRANSFERASE FTASE; FTASE; FTASE, PFT, PFTASE, FARNESYLTRANSFERASE, FARNESYL 2 TRANSFERASE, CAAX, RAS, CANCER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1e96	B	135	278	1.4e-09	0.15	0.48		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	189	322	8e-10	0.40	0.76		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	229	379	4.8e-09	0.14	0.98		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	290	417	4.8e-09	0.05	0.86		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e96	B	62	244	0.00016	0.12	0.21		RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1; CHAIN: A; NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) CHAIN: B;	SIGNALLING COMPLEX RAC1; P67PHOX; SIGNALLING COMPLEX, GTPASE, NADPH OXIDASE, PROTEIN-PROTEIN 2 COMPLEX, TPR MOTIF
1238	1e1r	A	133	247	6.4e-15	0.38	0.47		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1e1r	A	161	252	6.4e-15	0.24	1.00		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1e1r	A	195	283	1.6e-10	0.02	0.96		TPR2A-DOMAIN OF HOP;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	228	326	4.8e-12	0.47	0.99		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	262	355	3.2e-13	0.27	0.74		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	28	117	4.8e-11	0.13	0.29		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	334	419	4.8e-12	0.54	0.55		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elr	A	93	185	1.1e-11	0.31	0.33		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1238	1elw	A	135	221	1.1e-13	0.46	0.99		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	153	262	1.3e-12	0.47	0.96		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	196	296	3.2e-10	0.63	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1238	1elw	A	236	332	4.8e-13	0.76	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	25	122	4.8e-10	0.32	0.57		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	2	99	6.4e-14	0.25	0.03		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	304	408	3.2e-15	0.23	0.98		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	342	419	1.1e-11	0.29	0.21		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1elw	A	61	155	6.4e-10	0.32	0.82		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1238	1fch	A	166	413	9.6e-38	0.32	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	313	420	3.2e-09	0.07	0.96		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING	SIGNALING PROTEIN PEROXISOMAL RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PEPTIDE; CHAIN: C, D;	PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	34	273	6.4e-31	0.48	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	7	220	1.3e-29	0.38	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1238	1fch	A	98	345	4.8e-29	0.46	1.00		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISOMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRA TRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1241	1edh	A	34	152	3.2e-20	0.10	0.55		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	52	253	6.8e-27	-0.19	0.76		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1edh	A	83	255	4.8e-17	0.21	0.64		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1241	1nci	B	206	253	5.1e-06	-0.07	0.04		N-CADHERIN; INCI 3	CELL ADHESION PROTEIN
1241	1nci	B	56	152	1.7e-05	0.15	0.31		N-CADHERIN; INCI 3	CADHERIN INCI 13
1241	1ncj	A	34	152	1.4e-21	-0.20	0.28		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN
1241	1ncj	A	43	253	1.7e-21	-0.03	0.65		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1241	1ncj	A	90	255	6.4e-17	-0.20	0.35		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1241	1qu0	A	358	549	3.4e-20	-0.08	0.40		LAMININ ALPHA2 CHAIN; CHAIN: A, B, C, D;	METAL BINDING PROTEIN BETA SANDWICH, CALCIUM-BINDING PROTEIN, METAL BINDING 2 PROTEIN
1241	1suh		43	154	1.7e-07	-0.22	0.04		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1246	1a5e		132	262	3.4e-30	0.56	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		166	330	3.4e-30	0.40	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		202	359	5.1e-29	0.84	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	385	1.5e-29	0.39	0.93		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1a5e		233	393	3.4e-30			66.97	TUMOR SUPPRESSOR	ANTI-ONCOGENE CELL CYCLE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1awc	B	145	298	1e-43	1.05	1.00		P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE, REPEAT, ANK REPEAT
1246	1awc	B	14	165	1e-39	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	150	298	9.6e-41	0.97	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	17	165	1.6e-38	0.93	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	lawc	B	183	332	3.4e-39	0.84	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	184	332	9.6e-35	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	212	362	1e-40	0.77	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	212	363	1e-43			90.97	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA) DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	lawc	B	217	395	3.2e-32	0.21	0.23		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	3	132	1.6e-33	0.88	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	45	199	8.5e-39	0.55	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1awc	B	50	199	9.6e-37	0.68	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1246	1bd8		145	301	8e-30			87.65	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1246	1bd8		153	301	8e-30	0.38	1.00		P19INK4D CDK4/6 INHIBITOR;	TUMOR SUPPRESSOR TUMOR

SEQ ID NO.	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: NULL;	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1246	1bi7	B	244	365	1.7e-28	0.57	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1246	1blx	B	114	304	3.4e-38	0.10	0.10		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	13	170	1.7e-39	0.93	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	147	303	6.8e-40			78.94	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	183	338	3.4e-38	0.73	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
1246	1blx	B	215	368	1.7e-38	0.89	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEIN/KINASE) COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	50	205	1.5e-38	0.70	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1blx	B	82	237	6.8e-40	1.03	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1246	1bu9	A	144	310	6.8e-37	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	150	303	1.6e-36	0.97	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	17	170	9.6e-37	0.87	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1bu9	A	181	338	1e-35	0.61	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	184	367	8e-33	0.25	0.99		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	215	373	3.4e-35	0.63	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	243	394	6.8e-33	0.79	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	3	174	3.4e-37	0.47	0.51		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	44	205	1.7e-39	0.94	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1246	1bu9	A	9	177	1.7e-39			89.81	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	lihb	A	150	302	6.4e-36	0.88	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	HORMONE/GROWTH FACTOR CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	lihb	A	17	169	3.2e-36	0.78	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	lihb	A	184	366	3.2e-32	0.28	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	lihb	A	81	236	3.2e-36			83.68	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1246	likn	D	12	186	4.8e-35	0.47	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	likn	D	179	346	1.6e-30	0.20	0.92		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	likn	D	212	404	1.6e-34	0.22	0.35		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	likn	D	45	232	8e-43	0.18	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	1ikn	D	45	253	8e-43			80.97	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1246	1myo		12	130	9.6e-25			68.11	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1246	1nfi	E	113	311	1.7e-48	0.69	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nfi	E	11	186	1.4e-35	0.81	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nfi	E	143	338	5.1e-47	0.55	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nfi	E	177	367	1.7e-48	0.62	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	1nfi	E	178	346	4.8e-30	0.65	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1246	Infi	E	17	170	3.4e-38	0.85	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	210	404	9.6e-35	0.26	0.21		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	215	394	1.5e-44	0.53	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	43	238	1.7e-51	0.53	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	43	242	1.7e-51			89.07	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	44	232	1.6e-42	0.74	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1246	Infi	E	82	278	5.1e-50	0.66	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1246	1sw6	A	76	320	1.3e-21			60.99	REGULATORY PROTEIN SWI6; CHAIN: A, B;	ANKYRIN 2 REPEAT HELIX TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
1246	1ycs	B	214	398	3.2e-18			69.71	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN; PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1250	1cun	A	375	591	5.1e-12	-0.03	0.29		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1cun	A	436	651	5.1e-07	0.02	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1250	1hae		120	150	0.0051	0.07	0.11		HEREGULIN-ALPHA; CHAIN: NULL;	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
1250	1hre		120	150	0.0051	0.13	0.25		GROWTH FACTOR HEREGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1252	1d4v	A	326	426	5.1e-10	0.10	-0.14		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
1252	1dan	L	351	449	8e-09	0.06	-0.13		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1252	1dx5	I	233	346	3.2e-12	0.02	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1252	1dx5	I	268	394	6.4e-15	0.03	-0.20		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1252	1dx5	I	308	436	1.1e-12	0.10	-0.19		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1252	1emn		307	395	1.6e-13	0.24	0.04		FIBRILLIN; CHAIN: NULL;	ANTIFIBRINOLYTIC COMPLEX MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1252	1emn		351	431	3.2e-10	0.08	-0.19		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1252	1klo		225	419	8.5e-39	0.17	0.93		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		234	411	8.5e-39			132.10	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		293	452	1.6e-20	0.40	0.51		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1klo		358	496	3.2e-18	-0.00	-0.03		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1252	1pfx	L	351	441	3.2e-09	0.10	-0.17		FACTOR IXA; CHAIN: C, L, I; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN
1252	1skz		319	414	3.4e-17	0.34	-0.14		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1252	1skz		355	425	5.1e-10	0.16	0.19		ANTISTASIN; CHAIN: NULL;	INHIBITOR, THROMBOSIS SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1252	1xka	L	355	448	3.2e-09	0.14	-0.18		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1252	4mt2		368	428	1.3e-09	-0.05	0.00		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
1252	9wga	A	298	492	4.8e-15	0.04	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1253	1one	A	11	134	9.6e-61	0.25	1.00		ENOLASE; CHAIN: A, B;	LYASE 2-PHOSPHO-D-GLYCERATE HYDROLASE; LYASE, GLYCOLYSIS
1253	1pdz		11	137	8e-63	0.15	1.00		ENOLASE; IPDZ 4 CHAIN: NULL; IPDZ 5	LYASE (CARBON-OXYGEN) 2- PHOSPHO-D-GLYCERATE DEHYDRATASE; IPDZ 6
1256	1kpf		53	163	9.6e-41	0.96	1.00		PROTEIN KINASE C INTERACTING PROTEIN; CHAIN: NULL;	PROTEIN KINASE INHIBITOR PKC- 1, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKC-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	1kpf		53	163	9.6e-41			144.01	PROTEIN KINASE C	PROTEIN KINASE INHIBITOR PKC-1

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									INTERACTING PROTEIN; CHAIN: NULL;	1, PROTEIN KINASE C INHIBITOR 1, HINT PROTEIN KINASE INHIBITOR, PKC-1, HIT PROTEIN FAMILY, 2 HISTIDINE TRIAD PROTEIN FAMILY, NUCLEOTIDYL HYDROLASE, 3 NUCLEOTIDYL TRANSFERASE
1256	4rhv		47	163	6.4e-41			147.29	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1256	4rhv		52	163	6.4e-41	0.86	1.00		HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN; CHAIN: NULL;	NUCLEOTIDE-BINDING PROTEIN HINT; NUCLEOTIDE-BINDING PROTEIN
1257	1a5e		39	151	1.4e-21	0.27	0.48		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		39	154	8e-26	0.80	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		61	162	3.4e-25	0.65	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1a5e		6	121	4.8e-18	0.16	0.40		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1257	1awc	B	39	164	6.4e-37	0.61	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1257	1awc	B	4	154	9.6e-40	0.40	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1257	1bd8		7	157	1.3e-31	0.48	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1257	1bi7	B	39	154	3.2e-26	0.62	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1bi7	B	6	121	8e-19	0.22	0.35		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1257	1blx	B	39	164	1.7e-32	0.82	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1257	1blx	B	7	157	1.6e-30	0.38	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	(INHIBITOR PROTEIN/KINASE) COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1257	1bu9	A	6	159	8e-37	0.34	0.88		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1257	1d9s	A	39	154	1.6e-26	0.70	1.00		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1d9s	A	6	127	3.2e-20	0.42	0.95		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1257	1dcq	A	2	91	6.4e-15	0.41	0.80		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	1dcq	A	71	157	1.1e-17	0.05	0.99		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN
1257	1ihb	A	6	158	4.8e-36	0.52	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1257	1ihb	A	73	163	8e-18	0.47	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR

SEQ ID NO:	PDB ID	CHAIN NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	likn	D	4	162	8e-38	0.08	0.84		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D; MYOTROPHIN; CHAIN: NULL	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1257	lmyo		35	152	3.2e-26			52.27	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	lmyo		40	156	3.2e-26	0.32	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	lmyo		5	106	6.4e-24	0.22	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	lmyo		74	164	1.1e-23	0.04	1.00		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1257	lnfi	E	4	162	1.6e-38	0.39	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1257	lycs	B	12	95	1.4e-19	0.04	0.86		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1257	lycs	B	39	154	1.6e-25	0.24	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1257	1ycs	B	73	161	1.6e-22	0.44	1.00		P53; CHAIN: A; 53BP2; CHAIN: B;	ONCOGENE/ANKYRIN REPEATS) COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1258	1afb	1	3	183	3.4e-20			52.08	MANNOSE-BINDING PROTEIN-A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LECTIN CL-QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22
1258	1bj3	A	31	180	8e-34	0.42	0.11		COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1258	1bj3	A	34	181	8e-34			61.48	COAGULATION FACTOR IX-BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-BINDING PROTEIN B; CHAIN: B;	COLLAGEN BINDING PROTEIN IX-BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN
1258	1c3a	A	31	185	6.4e-28	0.20	0.89		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS
1258	1c3a	B	31	183	1.4e-30	0.03	0.01		FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT; CHAIN: B	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1258	1dv8	A	31	180	6.4e-28	0.72	0.68		ASIALOGLYCOPROTEIN RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN HEPATIC LECTIN HI; C-TYPE LECTIN CRD
1258	1e5u	I	52	80	0.0093	-0.69	0.57		INTIMIN; CHAIN: I;	INTIMIN INT190; INTIMIN, ESCHERICHIA COLI, CELL ADHESION, OUTER MEMBRANE 2 PROTEIN, NMR SPECTROSCOPY
1258	1egg	B	29	187	1.6e-29	0.41	0.36		MACROPHAGE MANNOSE RECEPTOR; CHAIN: A, B;	SUGAR BINDING PROTEIN C-TYPE LECTIN, MANNOSE RECEPTOR
1258	1esl		44	213	4.8e-30	0.45	0.89		CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258	1esi		45	220	4.8e-30			60.26	CELL ADHESION PROTEIN E-SELECTIN (LECTIN AND EGF DOMAINS, RESIDUES 1 - 157) IESL 3 (FORMERLY KNOWN AS ELAM-1) IESL 4	
1258	1f00	I	52	80	0.0093	-0.19	0.40		INTIMIN; CHAIN: I;	CELL ADHESION IMMUNOGLOBULIN-LIKE FOLD, C-TYPE LECTIN-LIKE FOLD
1258	1htn		12	184	1.3e-23			68.61	TETRALECTIN; CHAIN: NULL;	LECTIN TETRALECTIN, PLASMINOGEN BINDING, KRINGLE 4, ALPHA-HELICAL 2 COILED COIL, C-TYPE LECTIN, CARBOHYDRATE RECOGNITION DOMAIN
1258	1hup		8	183	6.4e-21			50.48	MANNOSE-BINDING PROTEIN; 1HUP 4 CHAIN: NULL; 1HUP 5	C-TYPE LECTIN ALPHA-HELICAL COILED-COIL 1HUP 12
1258	1ixx	A	31	180	4.8e-32	0.21	0.21		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1ixx	A	34	181	4.8e-32			58.55	COAGULATION FACTORS	COAGULATION FACTOR BINDING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1bx	B	31	183	1.3e-29	0.24	0.45		COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1ix	B	34	183	1.3e-29			53.06	COAGULATION FACTORS IX/X-BINDING PROTEIN; CHAIN: A, B, C, D, E, F;	COAGULATION FACTOR BINDING IX/X-BP COAGULATION FACTOR BINDING, C-TYPE LECTIN, GLA-DOMAIN 2 BINDING, C-TYPE CRD MOTIF, LOOP EXCHANGED DIMER
1258	1lit		31	182	1.6e-31	0.51	0.30		LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
1258	1lit		31	183	1.6e-31			71.84	LITHOSTATHINE; CHAIN: NULL	PANCREATIC STONE INHIBITOR, PANCREATIC STONE INHIBITOR, LECTIN
1258	1qdd	A	18	183	1.6e-31			72.35	LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN, PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1qdd	A	31	182	1.6e-31	0.65	0.52		LITHOSTATHINE; CHAIN: A;	METAL BINDING PROTEIN, PANCREATIC STONE PROTEIN, PSP; PANCREATIC STONE INHIBITOR, LITHOSTATHINE
1258	1rtm	1	3	183	5.1e-19			50.72	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) 1RTM 3 1RTM 96	
1258	1tn3		28	184	1.2e-24			59.80	TETRALECTIN; CHAIN: NULL;	LECTIN TETRALECTIN, PLASMINOGEN BINDING, KRINGLE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										4, C-TYPE LECTIN, 2 CARBOHYDRATE RECOGNITION DOMAIN
1258	2afp	A	29	179	1.6e-27	-0.06	0.54		SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN; SOLUTION BACKBONE FOLD, C-2 TYPE LECTIN, ANTIFREEZE PROTEIN
1259	1dap	A	1	33	4.8e-05	-0.51	0.13		DIAMINOPIMELIC ACID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE DAPDH; NADP, DEHYDROGENASE, D-AMINO ACID DEHYDROGENASE, LYSINE 2 BIOSYNTHESIS, ASYMMETRIC DIMER, OXIDOREDUCTASE
1259	3gpd	R	2	336	0			491.59	OXIDOREDUCTASE (NAD\$(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	
1259	3gpd	R	3	336	0	0.93	1.00		OXIDOREDUCTASE (NAD\$(A)-ALDEHYDE(D)) D-GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (E.C.1.2.1.12) 3GPD 4	
1263	1a7c	A	82	463	4.8e-91			115.78	PLASMINOGEN ACTIVATOR INHIBITOR TYPE I; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
1263	1as4	A	88	430	0	0.25	0.96		ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	1as4	A	90	438	0			104.85	ANTICHYMOTRYPSIN; CHAIN: A, B;	ANTICHYMOTRYPSIN SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
1263	1ath	B	101	464	1.3e-96			102.92	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1263	1ath	B	85	464	1.3e-96	0.23	1.00		HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1263	1by7	A	86	463	0	0.68	1.00		PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
1263	1by7	A	86	463	0			101.02	PLASMINOGEN ACTIVATOR INHIBITOR-2; CHAIN: A;	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING
1263	1d5s	B	433	463	1.3e-09	-0.75	0.04		PI-ARG ANTITRYPSIN; CHAIN: A; P1-ARG ANTITRYPSIN; CHAIN: B;	HYDROLASE INHIBITOR SERPIN FOLD, RCL CLEAVAGE, A BETA SHEET POLYMERISATION
1263	1db2	A	83	463	3.2e-94			120.11	PLASMINOGEN ACTIVATOR INHIBITOR-1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
1263	1ezx	A	86	432	0	0.23	0.80		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1- ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1- ANTITRYPSIN, 2 TRYPSIN
1263	1hle	A	85	426	3.2e-98	0.38	1.00		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
1263	1hle	A	85	432	3.2e-98			84.90	HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
1263	1ova	A	80	463	0			126.84	SERPIN OVALBUMIN (EGG ALBUMIN) IOVA 3	
1263	1ova	A	87	463	0	0.62	1.00		SERPIN OVALBUMIN (EGG	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	1qlp	A	86	463	0	0.49	1.00		ALBUMIN; IOVA 3 ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE.
1263	1qlp	A	88	466	0			146.76	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1263	1qmb	B	433	463	4.8e-09	-0.75	0.12		ALPHA-1-ANTITRYPSIN; CHAIN: A, B;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-P1; SERPIN, ANTITRYPSIN, POLYMER, CLEAVED
1263	1qmn	A	88	464	0	0.44	1.00		ALPHA-1- ANTITRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
1263	1sek		80	463	3.2e-85			102.05	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
1263	2ant	I	47	466	0			139.88	ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
1263	2ant	I	49	464	0	0.48	1.00		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1263	2ant	L	59	466	0			125.53	ANTITHROMBIN; CHAIN: L, I;	INHIBITOR
1263	2ant	L	81	464	0	0.63	1.00		ANTITHROMBIN; CHAIN: L, I;	SERPIN SERPIN, HEPARIN, INHIBITOR
1264	1aln	A	25	218	6.4e-92	0.93	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	SERPIN SERPIN, HEPARIN, INHIBITOR
1264	1aln	A	25	219	1.2e-93			237.20	B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1aln	A	26	210	1.2e-93	1.19	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1264	1agd	A	25	218	3.2e-92	0.97	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	25	219	3.2e-92			239.77	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1264	1agd	A	26	210	8.5e-92	0.98	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1264	1duz	A	25	218	1.6e-88	1.03	1.00		(GGKKYKL - INDEX PEPTIDE); CHAIN: C; HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	HISTOCOMPATIBILITY COMPLEX
1264	1efx	A	25	218	9.6e-91	1.13	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1efx	A	26	210	8.5e-93	1.29	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1264	1hoc	A	25	218	1.6e-84			206.63	HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING IHOC 3 OF H-2D-B, B2- MICROGLOBULIN, AND A 9- RESIDUE PEPTIDE IHOC 4	
1264	1hsa	A	25	218	3.2e-91	0.91	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN IHS A 3 /HLA- B(ASTERISK)2705\$ IHS A 4	
1264	1hsa	A	25	219	3.2e-91			231.27	HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1264	1hsb	A	25	218	3.2e-89	1.15	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1264	1hsb	A	25	219	3.2e-89			226.78	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1264	1mhe	A	26	219	4.8e-88			209.47	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE 3 NON-CLASSICAL MHC, CLASS IB MHC IMMUNE SYSTEM
1264	1qqd	A	26	218	6.4e-89	1.17	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1264	1tmc	A	25	199	9.6e-81			257.75	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1265	1aln	A	25	212	0	0.82	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	1aln	A	25	213	0			222.84	B*3501; CHAIN: A, B; PEPTIDE VPLRPMY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1265	lagd	A	25	212	0	0.93	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	lagd	A	25	213	0			242.14	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1265	lefx	A	25	212	4.8e-100	0.96	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1265	lhsa	A	25	212	1.6e-100	1.04	1.00		HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1265	1hsa	A	25	213	1.6e-100			212.48	ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1265	1qgd	A	26	212	1.3e-98	0.83	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	IMMUNE SYSTEM
1265	1tmc	A	25	199	3.2e-93	1.00	1.00		LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1265	1tmc	A	25	199	3.2e-93			245.23	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1266	1aln	A	22	210	4.8e-97	0.88	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1266	1aln	A	22	210	4.8e-97			202.13	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	1agd	A	22	210	1.1e-97	0.92	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1266	1agd	A	22	210	1.1e-97			212.14	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1266	1duz	A	22	208	4.8e-95	0.88	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1266	1efx	A	22	210	3.2e-96	1.08	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1266	1hsa	A	22	210	3.2e-96	0.89	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1266	1hsa	A	22	210	3.2e-96			195.27	B(ASTERISK)2705\$ I HSA 4 HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4 HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1266	1hsb	A	22	208	4.8e-96	0.87	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1266	1hsb	A	22	210	4.8e-96			189.34	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1266	1qqd	A	23	210	3.2e-94	0.89	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1266	1tmc	A	22	197	4.8e-90	0.98	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1266	1tmc	A	22	197	4.8e-90			228.77	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1267	1aln	A	25	214	6.4e-100	1.01	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1267	1aln	A	25	214	6.4e-100			206.29	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1267	lagd	A	25	214	1.6e-100	0.95	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	lagd	A	25	214	1.6e-100			193.54	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1267	lduz	A	25	214	3.2e-97	0.96	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1267	lefx	A	25	214	1.6e-98	0.91	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E; HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1267	lhas	A	25	214	1.6e-99	1.02	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1267	lhas	A	25	214	1.6e-99			198.64	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1267	lhasb	A	25	214	1.1e-98	0.98	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1267	lhasb	A	25	214	1.1e-98			190.28	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1267	lqgd	A	26	214	4.8e-97	0.95	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C; HISTOCOMPATIBILITY	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1267	ltmc	A	25	200	6.4e-91	0.91	1.00		HISTOCOMPATIBILITY	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1267	1tmc	A	25	200	6.4e-91			227.42	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1268	1aln	A	25	301	0	0.83	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	1aln	A	25	301	0			381.69	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1268	1agd	A	25	301	0	0.79	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYK1 - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1268	1agd	A	25	301	0			382.18	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1268	1dn2	A	224	314	0.00034	-0.28	0.00		(GGKKKKYL - INDEX PEPTIDE); CHAIN: C; IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	HISTOCOMPATIBILITY COMPLEX
1268	1duz	A	25	300	0	0.83	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
1268	1efx	A	25	303	0	0.83	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1268	1hsa	A	25	301	0	0.80	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1268	1hsa	A	25	301	0			381.68	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1268	1hsb	A	25	295	0	0.82	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I, HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1268	1hsb	A	25	295	0			416.11	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1268	ligt	B	224	308	1.6e-05	0.26	0.71		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1268	1mco	H	189	310	1.7e-05	0.09	0.23		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1268	1mco	H	220	314	6.8e-06	0.30	0.48		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1268	1qdd	A	26	299	0	0.63	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1269	1aln	A	25	285	0	0.88	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1269	1aln	A	25	288	0			279.39	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1269	lagd	A	25	285	0	0.87	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GKKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	lagd	A	25	288	0			278.31	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GKKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1269	lduz	A	25	285	0	0.93	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1269	lefx	A	25	285	0	0.94	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E; HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1269	lhas	A	25	285	0	0.93	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1269	lhas	A	25	288	0			284.65	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705\$ 1HSA 4	
1269	lhas	A	25	285	0	0.83	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1269	1hsb	A	25	288	0				HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1mhe	A	26	285	0	0.70	1.00	302.23	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1269	1mhe	A	26	288	0			253.44	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC
1269	1qqd	A	26	285	0	0.86	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1269	1tmc	A	25	200	8e-88	0.97	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1269	1tmc	A	25	200	8e-88			257.46	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1271	1aln	A	25	218	1.4e-94	0.95	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	25	219	5.1e-96			239.16	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1aln	A	26	210	5.1e-96	1.03	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1271	1agd	A	25	218	3.2e-95	1.03	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV.

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1agd	A	25	219	3.2e-95			243.91	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKKYL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1271	1duz	A	25	218	3.2e-91	0.93	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1271	1efx	A	25	218	1.6e-93	0.95	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1efx	A	26	210	1e-95	1.16	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1271	1hsa	A	25	218	4.8e-94	0.99	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1271	1hsa	A	25	219	4.8e-94			235.85	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I	

SEQ ID NO.	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HISTOCOMPATIBILITY ANTIGEN I HSA 3 / HLA-B(ASTERISK)2705S I HSA 4	
1271	lfsb	A	25	218	4.8e-92	1.11	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1271	lfsb	A	25	219	4.8e-92			238.52	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE IHSB 3 ANTIGEN) IHSB 4	
1271	lmhe	A	26	218	1.6e-92	0.94	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1271	lmhe	A	26	219	1.6e-92			218.16	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-CLASSICAL MHC, CLASS IB MHC
1271	lqgd	A	26	218	1.6e-92	0.95	1.00		HISTOCOMPATIBILITY	IMMUNE SYSTEM

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1271	ltmc	A	25	199	1.4e-83			267.94	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1272	lain	A	25	213	8e-91	0.92	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1272	lain	A	25	213	8e-91			150.68	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1272	lagd	A	25	213	3.2e-91	0.79	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1272	lagd	A	25	213	3.2e-91			152.02	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1272	1duz	A	25	213	6.4e-90	0.75	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1272	1efx	A	25	213	6.4e-91	0.89	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2- MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1272	1hsa	A	25	213	1.6e-90	0.92	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1272	1hsa	A	25	213	1.6e-90			151.46	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA- B(ASTERISK)2705\$ I HSA 4	
1272	1hsb	A	25	213	3.2e-91	0.87	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1272	1hsb	A	25	213	3.2e-91			178.43	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1272	1mhe	A	26	213	4.8e-87	0.92	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC
1272	1mhe	A	26	213	4.8e-87			144.34	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC
1272	1qgd	A	26	213	8e-89	0.67	1.00		HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)- CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1272	1tmc	A	25	201	9.6e-87	0.83	1.00		HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1272	1tmc	A	25	205	9.6e-87			215.19	HISTOCOMPATIBILITY ANTIGEN TRUNCATED	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 ITMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) ITMC 4	
1273	1aln	A	25	205	6.4e-97	0.98	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1273	1aln	A	25	219	6.4e-97			221.84	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1273	1agd	A	25	205	3.2e-97	1.14	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1273	1agd	A	25	219	3.2e-97			223.96	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1273	1duz	A	25	205	1.1e-95	1.27	1.00		HLA-A*0201; CHAIN: A, D; BETA-2 MICROGLOBULIN; CHAIN: B, E; HTLV-1 OCTAMERIC TAX PEPTIDE; CHAIN: C, F;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD
1273	1efx	A	25	205	4.8e-97	1.17	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E; HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1273	1hsa	A	25	205	1.6e-96	1.12	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1273	1hsa	A	25	219	1.6e-96			222.04	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN I HSA 3 /HLA-B(ASTERISK)2705\$ I HSA 4	
1273	1hsb	A	25	205	1.6e-97	1.03	1.00		HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1273	1hsb	A	25	218	1.6e-97			245.70	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE I HSB 3 ANTIGEN) I HSB 4	
1273	1qqd	A	26	205	1.1e-95	1.07	1.00		HISTOCOMPATIBILITY LEUCOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C; HISTOCOMPATIBILITY	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1273	1tmc	A	25	199	1.6e-93	1.25	1.00			

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1273	1tmc	A	25	199	1.6e-93			273.81	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-A*W68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1274	1buo	A	1	126	1.6e-22	0.30	1.00		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1buo	A	5	128	3.4e-28	0.41	0.99		PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION
1274	1gof		291	458	1.1e-11	0.05	0.17		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1274	lgof		383	495	1.6e-08	0.27	0.13		(E.C.1.1.3.9) (PH 4.5) IGOF 3 OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) IGOF 3	
1275	lcun	A	170	385	6.8e-09			65.74	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1275	lquu	A	180	415	3.4e-12			59.43	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1275	lsig		130	416	5.1e-05			76.16	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1276	labr	B	413	552	1.4e-09	0.45	0.40		COMPLEX (GLYCOSIDASE/CARBOHYDRATE) ABRIN-A COMPLEXED WITH TWO SUGAR CHAINS LABR 3	
1276	lce7	B	441	552	1.2e-15	0.16	0.21		RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIBOSOME RIBOSOME-INACTIVATING PROTEIN TYPE II
1276	lce7	B	450	543	0.00011	-0.25	0.13		RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: A; RIBOSOME-INACTIVATING PROTEIN TYPE II; CHAIN: B	RIBOSOME RIBOSOME-INACTIVATING PROTEIN TYPE II
1276	lqgq	A	123	345	6.4e-22	0.09	0.28		SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN	TRANSFERASE GLYCOSYLTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1276	1xyf	A	441	543	1.6e-16	-0.02	0.66		CHAIN: A; ENDO-1,4-BETA-XYLANASE; CHAIN: A, B;	HYDROLASE XYLAN DEGRADATION
1276	2aai	B	441	543	1.3e-07	-0.31	0.03		GLYCOSIDASE RICIN (E.C.3.2.2.22) 2AAI 3	
1279	2ak3	A	1	38	1.3e-16	-0.87	0.98		TRANSFERASE (PHOSPHOTRANSFERASE) ADENYLATE KINASE ISOENZYME-3 (GTP: AMP PHOSPHOTRANSFERASE) 2AK3 3 (E.C.2.7.4.10) 2AK3 4	
1280	12e8	H	59	253	1.3e-38	0.01	0.21		2E8 (GGI=KAPPA=) ANTIBODY; CHAIN: L, H, M, P; 29G11 FAB; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
1280	1a0q	H	50	254	6.4e-37			61.67	29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY, ESTERASE
1280	1a0q	H	59	253	6.4e-37	-0.31	0.27		29G11 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, ESTERASE
1280	1a3r	H	50	256	1.3e-36			60.58	IGG2A; CHAIN: L, H; HUMAN RHINOVIRUS CAPSID PROTEIN VP2; CHAIN: P;	COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE) ANTIBODY 8F5; IMMUNOGLOBULIN, ANTIBODY, RHINOVIRUS, NEUTRALIZATION, 2 CONTINUOUS EPTOPE, COMPLEX (IMMUNOGLOBULIN/VIRAL PEPTIDE)
1280	1a4j	L	51	252	9.6e-37	-0.11	0.17		IMMUNOGLOBULIN, DIELS ALDER CATALYTIC ANTIBODY; CHAIN: L, H, A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
1280	1a5f	H	48	256	3.2e-35			61.06	MONOCLONAL ANTILE- SELECTIN 7A9 ANTIBODY; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB, ANTIBODY, ANTI-E-SELECTIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1280	1adq	L	50	255	1.1e-37	-0.04	0.00		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1280	1afv	H	52	253	4.8e-37	0.08	0.58		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV. CAPSID PROTEIN, 2 P24
1280	1axt	H	51	256	4.8e-33			56.82	IMMUNOGLOBULIN IGG2A; CHAIN: L, H;	IMMUNOGLOBULIN ANTIBODY FAB, CATALYST, ALDOLASE REACTION
1280	1b2w	L	51	258	8e-39	0.04	-0.07		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRUCTURE, GAMMA-3 INTERFERON, IMMUNE SYSTEM
1280	1b4j	L	51	258	1.4e-37	0.00	0.09		ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY STRUCTURES, GAMMA-INTERFERON
1280	1b6d	A	51	252	4.8e-37	-0.12	0.13		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN, KAPPA LIGHT-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1280	1bjl	L	51	252	8e-38	0.09	-0.09		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W; MONOCLONAL ANTIBODY MRK-16 (LIGHT CHAIN); CHAIN: A, C; MONOCLONAL ANTIBODY MRK-16 (HEAVY CHAIN); CHAIN: B, D;	CHAIN DIMER HEADER COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF: COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR IMMUNE SYSTEM IMMUNOGLOBULIN, IMMUNE SYSTEM
1280	1bln	A	47	252	4.8e-35			57.09	IMMUNOGLOBULIN OPG2 FAB, CONSTANT DOMAIN; CHAIN: L; IMMUNOGLOBULIN OPG2 FAB, VARIABLE DOMAIN; CHAIN: H;	IMMUNE SYSTEM
1280	1bm3	H	51	258	1.6e-34			57.73	COMPLEX (ANTIBODY/ANTIGEN) HYHEL-5 FAB COMPLEXED WITH BOBWHITE QUAIL LYSOZYME	IMMUNE SYSTEM
1280	1bql	H	50	255	3.2e-36			59.53	IBQL 3 IBQL 95	IMMUNOGLOBULIN
1280	1bz7	B	51	250	1.6e-26			57.49	ANTIBODY R24 (LIGHT CHAIN); CHAIN: A; ANTIBODY R24 (HEAVY CHAIN); CHAIN: B;	IMMUNE SYSTEM ANTIBODY (FAB FRAGMENT), IMMUNE SYSTEM
1280	1ce1	L	51	252	9.6e-37	0.11	-0.03		CAMPATH-1H LIGHT CHAIN; CHAIN: L; CAMPATH-1H HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1280	1cr9	H	59	255	8e-39	-0.12	0.60		FAB ANTIBODY LIGHT CHAIN; CHAIN: L; FAB ANTIBODY HEAVY CHAIN; CHAIN: H;	IMMUNE SYSTEM ANTI-PRION FAB 3F4; ANTI-PRION FAB 3F4 ANTI-PRION ANTIBODY, FAB 3F4
1280	1fbi	H	48	255	1.6e-36			56.80	COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1280	1flr	H	51	256	3.2e-33			56.39	MONOCLONAL ANTIBODY F9.13.7 (IGG1) IFBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) IFBI 4 4-4-20 (IG*G2A=KAPPA=) FAB FRAGMENT; 1FLR 5 CHAIN: L ₂ H ₂ 1FLR 6	IMMUNOGLOBULIN
1280	1fvd	A	51	258	1.4e-37	0.11	-0.12		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1280	1fvd	B	51	258	6.4e-32			57.20	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	
1280	1hyx	L	47	255	1.3e-34			57.33	IMMUNOGLOBULIN 6D9; CHAIN: L ₂ H ₂	CATALYTIC ANTIBODY CATALYTIC ANTIBODY 6D9 CATALYTIC ANTIBODY, ESTER HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN
1280	1iai	H	48	254	4.8e-33			60.65	IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 1IAI 5 CHAIN: L ₂ H ₂ 1IAI 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); 1IAI 9 CHAIN: M.1 1IAI 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1280	1lge	H	51	258	1.6e-32			57.26	COMPLEX (ANTIBODY/BINDING PROTEIN) IGG1 FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) IIGC 5 PROTEIN G, STREPTOCOCCUS IIGC 15	
1280	1lge	L	47	258	8e-35			58.26	IMMUNOGLOBULIN IGG1 FAB' FRAGMENT (B1312) IIGF 3	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	ligy	B	59	253	1.6e-36	0.02	0.37		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1280	lkel	H	51	255	6.4e-34			57.31	2B84 FAB; CHAIN: L, H;	CATALYTIC ANTIBODY SULFIDE OXIDATION, MONOOXYGENASE, OXYGENATION, FAB, 2 IMMUNOGLOBULIN, CATALYTIC ANTIBODY
1280	lmlb	B	48	258	8e-36			56.48	IMMUNOGLOBULIN FAB D44.1 (IGG1,KAPPA) (BALB/C MOUSE, MONOCLONAL ANTIBODY) IMLB 5	
1280	lnct		178	254	0.0015	0.08	0.35		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1280	lngp	H	51	253	6.4e-37	-0.09	0.22		N1G9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN
1280	lsm3	H	51	256	1.6e-36			58.83	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	lsm3	H	59	253	1.6e-36	-0.09	0.41		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1280	lsm3	L	50	252	3.2e-30			56.66	SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1280	1tet	H	48	256	6.4e-36			57.32	IMMUNOGLOBULIN IGG1 MONOCLONAL FAB FRAGMENT (TE33) COMPLEX WITH CHOLERA 1TET 3 TOXIN PEPTIDE 3 (CTP3) 1TET 4	2 COMPLEX (ANTIBODY/PEPTIDE EPTOPE)
1280	1nm		178	254	0.0051	-0.05	0.05		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1280	1wej	H	59	253	3.2e-37	0.55	0.70		E8 ANTIBODY; CHAIN: L, H; CYTOCHROME C; CHAIN: F;	COMPLEX (ANTIBODY/ELECTRON TRANSPORT) FAB E8; CYT C, ANTIGEN; IMMUNOGLOBULIN, IGG1 KAPPA, FAB FRAGMENT, HORSE 2 CYTOCHROME C, COMPLEX (ANTIBODY/ELECTRON TRANSPORT)
1280	1wwc	A	164	254	0.0051	-0.18	0.01		NT-3 GROWTH FACTOR RECEPTOR TRKC; CHAIN: A;	TRANSFERASE TRK RECEPTOR, RECEPTOR TYROSINE KINASE, 3D-DOMAIN SWAPPING, 2 TRANSFERASE
1280	25c8	H	48	254	1.1e-37			57.06	IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1280	25c8	H	59	253	1.1e-37	0.11	0.53		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1280	2cgr	H	51	254	1.6e-31			57.12	IMMUNOGLOBULIN IGG2B (KAPPA) FAB FRAGMENT COMPLEXED WITH ANTIGEN 2CGR 3 N-(P-CYANOPHENYL)-N'-(DIPHENYLEMETHYL)	

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									GUANIDINEACETIC ACID 2CGR 4	
1280	2fgw	L	51	258	1.6e-38	0.00	-0.08		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
1280	2hmi	C	47	258	4.8e-33			56.78	HIV-1 REVERSE TRANSCRIPTASE; CHAIN: A, B; MONOCLONAL ANTIBODY 28; CHAIN: C, D; DNA; CHAIN: E, F;	COMPLEX (RT/DNA/FAB) HIV-1 RT; FAB 28; AIDS, HIV-1, RT, POLYMERASE
1280	7fab	H	49	255	3.2e-31			57.01	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
1284	1crk	A	1	46	3.2e-19	-0.83	0.27		CREATINE KINASE; CHAIN: A, B, C, D;	TRANSFERASE TRANSFERASE, CREATINE KINASE
1284	1qh4	A	1	46	4.8e-19	-0.83	0.30		CREATINE KINASE, B CHAIN; CHAIN: A, B, C, D;	TRANSFERASE BB-CK, BRAIN-TYPE CREATINE KINASE; BRAIN-TYPE CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, NEURODEGENERATIVE DISORDERS
1284	1qkl	A	1	46	6.4e-19	-0.83	0.33		CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL; CHAIN: A, B, C, D, E, F, G, H;	TRANSFERASE (CREATINE KINASE) UMTCK, MIA-CK; MITOCHONDRIAL CREATINE KINASE, CANCER, CELLULAR ENERGY 2 METABOLISM, GUANIDINO KINASE, MITOCHONDRIAL PERMEABILITY 3 TRANSITION, OCTAMER STABILITY
1284	2crk	A	1	46	1.4e-19	-0.83	0.19		CREATINE KINASE; CHAIN: A;	TRANSFERASE CREATINE KINASE,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										TRANSFERASE
1287	1bq0		5	69	1.1e-27	0.89	1.00		DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1bq0		5	78	1.1e-27			68.92	DNAJ; CHAIN: NULL;	CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
1287	1hdj		10	77	3.4e-30	0.77	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1287	1hdj		5	80	3.4e-30			83.03	HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1287	1hdj		7	69	1.6e-27	1.26	1.00		HUMAN HSP40; CHAIN: NULL;	MOLECULAR CHAPERONE HDJ-1; MOLECULAR CHAPERONE
1292	1pbw	A	112	300	6.4e-08			93.22	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1292	1pbw	B	112	314	8e-09			94.15	PHOSPHATIDYLINOSITOL 3-KINASE; CHAIN: A, B;	PHOSPHOTRANSFERASE RHOGAP DOMAIN; PHOSPHOTRANSFERASE, TPASE ACTIVATING PROTEIN, GAP, CDC42, 2 PHOSPHOINOSITIDE 3-KINASE, SH3 DOMAIN, SH2 DOMAIN, 3 SIGNAL TRANSDUCTION
1292	1rgp		99	288	4.8e-17			109.76	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE-ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1292	1rx4	A	105	302	1.1e-17			114.46	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN	COMPLEX(GTPASE ACTIVATN/PROTO-ONCOGENE)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									RHOA; CHAIN: B;	GTPASE-ACTIVATING PROTEIN RHO GAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1293	1bcq	M	112	281	9.6e-54			103.34	MEMBRANE-TYPE MATRIX METALLOPROTEINASE; CHAIN: M; METALLOPROTEINASE INHIBITOR; CHAIN: T;	COMPLEX (METALLOPROTEINASE/RECEPTOR) CDMT1-MMP; TIMP-2 MATRIX METALLOPROTEINASE, TISSUE INHIBITOR OF 2 METALLOPROTEINASES, PROTEINASE COMPLEX, PRO-GELATINASE A 3 ACTIVATOR, CRYSTAL STRUCTURE, COMPLEX 4 (METALLOPROTEINASE/RECEPTOR)
1293	1cge		110	254	8e-60			120.96	HYDROLASE (METALLOPROTEASE) COLLAGENASE (E.C.3.4.24.7) (CATALYTIC DOMAIN) CRYSTAL FORM I 1CGE 3	
1293	1ciz	A	107	272	4.8e-63			132.96	STROMELYSIN-1; CHAIN: A;	METALLOPROTEINASE MATRIX METALLOPROTEINASE-3; MATRIX METALLOPROTEINASE, MMP-3, NON-PEPTIDE INHIBITOR
1293	1ck7	A	25	699	0			647.13	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-LENGTH, METALLOPROTEINASE, 2 GELATINASE A
1293	1cxw	A	274	333	9.6e-14			90.80	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
1293	1fbl		107	449	3.2e-70			151.00	FIBROBLAST (INTERSTITIAL)	METALLOPROTEASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1293	1gen		474	699	9.6e-50			99.39	COLLAGENASE (MMP-1); IFBL 4 CHAIN: NULL; IFBL 5 GELATINASE A; CHAIN: NULL;	HYDROLASE (METALLOPROTEASE) MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE, HEMOPEXIN DOMAIN, HYDROLASE, METALLOPROTEASE
1293	1hfc		115	265	8e-60			117.07	METALLOPROTEASE FIBROBLAST COLLAGENASE (E.C.3.4.24.7) 1HFC 3	
1293	1mmq		107	279	8e-56			119.28	MATRILYSIN; 1MMQ 5 CHAIN: NULL; 1MMQ 6	METALLOPROTEASE MMP-9, PUMP-1, MATRIN; 1MMQ 7
1293	1pex		477	699	4.8e-63			84.70	COLLAGENASE-3; CHAIN: NULL;	METALLOPROTEASE MMP-13; C-TERMINAL HEMOPEXIN-LIKE DOMAIN OF MATRIX-METALLOPROTEINASE
1293	1qib	A	112	272	1.6e-57			144.06	GELATINASE A; CHAIN: A;	HYDROLASE MATRIX METALLOPROTEINASE-2; INHIBITOR, MATRIN, MATRIX METALLOPROTEINASE-2 (MMP-2), 2 GELATINASE A, METZINCIN, HYDROLASE
1293	1slm		44	272	1.6e-82			187.06	STROMELYSIN-1; CHAIN: NULL;	HYDROLASE MATRIX METALLOPROTEINASE-3, PROTEOGLYCANASE; HYDROLASE, METALLOPROTEASE, FIBROBLAST, COLLAGEN DEGRADATION
1293	830c	A	107	267	1.6e-59			138.28	MMP-13; CHAIN: A, B;	MATRIX METALLOPROTEASE MMP-13; MATRIX METALLOPROTEASE
1294	1ek7	A	25	432	0			419.38	GELATINASE A; CHAIN: A;	HYDROLASE MMP-2, 72KD TYPE IV COLLAGENASE; HYDROLASE (METALLOPROTEASE), FULL-

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1294	1cxw	A	274	333	3.2e-21			90.47	HUMAN MATRIX METALLOPROTEINASE 2; CHAIN: A;	LENGTH, METALLOPROTEINASE, 2 GELATINASE A HYDROLASE COL-2; BETA SHEET, ALPHA HELIX, HYDROLASE
1297	2ucz		400	562	3.2e-44			80.92	UBIQUITIN CONJUGATING ENZYME; CHAIN: NULL;	UBIQUITIN CONJUGATION UBC7; UBIQUITIN CONJUGATION, LIGASE, YEAST
1298	1b1h	A	1462	1834	8e-44			176.45	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1298	1fnf		1660	2042	8e-18			104.50	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1298	1ftb	B	1370	1645	3.2e-18			104.57	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1301	1agr	E	45	172	4.8e-48			146.45	GUANINE NUCLEOTIDE-BINDING PROTEIN GQD; CHAIN: A, D; RGS4; CHAIN: E, H;	COMPLEX (SIGNAL TRANSDUCTION/REGULATOR) G1-ALPHA-1; REGULATOR OF G-PROTEIN SIGNALLING 4; G1-ALPHA-1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN
1301	1agr	H	54	169	6.4e-43			133.76	GUANINE NUCLEOTIDE-	COMPLEX (SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									BINDING PROTEIN G(C); CHAIN: A, D; RGS4; CHAIN: E, H;	TRANSDUCTION/REGULATOR) G1-ALPHA-1; REGULATOR OF G-PROTEIN SIGNALLING 4; G1-ALPHA-1, HYDROLASE, SIGNAL TRANSDUCTION, RGS4, 2 COMPLEX (SIGNAL TRANSDUCTION/REGULATOR), GTP-BINDING, 3 GTPASE ACTIVATING PROTEIN
1301	1cmz	A	46	172	3.2e-46			121.40	GAIP (G-ALPHA INTERACTING) PROTEIN; CHAIN: A;	SIGNALING PROTEIN REGULATION GALPHA INTERACTING PROTEIN; GAIP, RGS, REGULATOR OF G PROTEIN, SIGNALING PROTEIN 2 REGULATION
1302	1a4i	A	5	235	4.8e-74			94.97	METHYLENETETRAHYDROFOLATE DEHYDROGENASE / CHAIN: A, B;	OXIDOREDUCTASE METHYLENETH DEHYDROGENASE / METHENYLTHF THF, BIFUNCTIONAL, DEHYDROGENASE, CYCLOHYDROLASE, FOLATE, 2 OXIDOREDUCTASE HEADER
1302	1b0a	A	1	235	8e-77			106.54	FOLD BIFUNCTIONAL PROTEIN; CHAIN: A;	OXIDOREDUCTASE, HYDROLASE FOLATE, DEHYDROGENASE, CYCLOHYDROLASE, BIFUNCTIONAL, 2 CHANNELLING, OXIDOREDUCTASE, HYDROLASE
1307	1awc	B	18	157	8e-34	-0.23	0.52		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1307	1awc	B	3	125	4.8e-29	-0.09	0.29		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABP BETA 1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1307	1bd8		21	160	8e-27	-0.01	0.19		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1307	1bi7	B	443	560	6.4e-17	0.14	0.04		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1307	1bli	B	21	160	6.4e-26	-0.17	0.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1307	1bli	B	50	183	1.3e-23	0.01	0.37		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1307	1bu9	A	1	130	6.4e-25	-0.12	0.15		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	(INHIBITOR PROTEIN/KINASE) HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR SUPPRESSOR, CYCLIN-2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1307	1d9s	A	443	567	1.6e-17	0.14	0.06		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1307	1ihb	A	18	161	1.3e-25	-0.12	0.10		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1ihb	A	1	129	3.2e-24	0.01	0.37		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1307	1myo		19	127	1.6e-20	0.14	0.01		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1314	1by2		26	138	1.1e-44			112.99	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1315	1ael	A	34	304	1.6e-66			73.73	TROPINONE REDUCTASE-I; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1315	1ae1	B	34	304	9.6e-68			76.92	TROPINONE REDUCTASE-I; CHAIN: A, B;	DEHYDROGENASE OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
1315	1bdb		35	314	1.6e-47			65.57	CIS-BIPHENYL-2,3-DIHYDRODIOL-2,3-DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE NAD-DEPENDENT OXIDOREDUCTASE, SHORT-CHAIN ALCOHOL 2 DEHYDROGENASE, PCB DEGRADATION
1315	1eyd	A	35	297	3.2e-54			69.13	CARBONYL REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE, OXIDOREDUCTASE
1315	1fds		38	319	4.8e-32			79.80	17-BETA-HYDROXYSTEROID-DEHYDROGENASE; CHAIN: NULL;	DEHYDROGENASE DEHYDROGENASE, 17-BETA-HYDROXYSTEROID
1315	1fmc	A	30	298	6.4e-66			82.26	7 ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: B;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE/REDUCTASE, BILE ACID CATABOLISM
1315	1hdc	A	35	306	4.8e-67			74.82	OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.1.53) 1HDC 3 COMPLEXED WITH CARBENOXOLONE 1HDC 4	
1315	1oaa		35	297	3.2e-21			65.22	SEPIAPTERIN REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE SEPIAPTERIN REDUCTASE, TETRAHYDROBIOPTERIN, OXIDOREDUCTASE
1315	1ybv	A	24	308	3.2e-61			82.44	TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE; OXIDOREDUCTASE
1315	2ae2	A	32	291	9.6e-65			76.67	TROPINONE REDUCTASE-II;	OXIDOREDUCTASE

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B;	OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO PSEUDOTROPINE, SHORT-CHAIN DEHYDROGENASE
1321	1pbk		224	339	1.3e-24			194.11	FKBP25; CHAIN: NULL;	ISOMERASE FKBP25 C-TERMINAL DOMAIN; FKBP12 HOMOLOGOUS DOMAIN OF FKBP25, ISOMERASE
1323	1am4	D	31	218	3.2e-43			50.20	P50-RHO GAP; CHAIN: A, B, C; CDC42HS; CHAIN: D, E, F;	COMPLEX (GTPASE-ACTIVATING/GTP-BINDING) COMPLEX (GTPASE-ACTIVATING/GTP-BINDING), GTPASE ACTIVATION
1323	1byu	A	29	244	3.2e-32			61.74	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	1byu	B	27	245	4.8e-33			64.26	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
1323	1cly	A	31	203	4.8e-64			79.57	RAS-RELATED PROTEIN RAP-1A; CHAIN: A; PROTO-ONCOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B;	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS
1323	1ctq	A	33	204	1.3e-64			93.92	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN
1323	1cxz	A	28	204	1.6e-50			52.92	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A; PKN; CHAIN: B;	SIGNALING PROTEIN PROTEIN-PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL
1323	1ibr	A	34	209	1.1e-31			60.48	RAN; CHAIN: A, C; IMPORTIN	SMALL GTPASE KARYOPHERIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1323	1kao		31	204	6.4e-61			91.54	BETA SUBUNIT; CHAIN: B, D; RAP2A; CHAIN: NULL;	BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR GTP-BINDING PROTEIN GTP-BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS
1323	1mhl		30	222	1.6e-51			62.77	RAC1; CHAIN: NULL;	GTP-BINDING GTP-BINDING, RHO GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY
1323	1rrp	C	31	227	1.1e-31			59.75	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN) COMPLEX (SMALL GTPASE/NUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1323	1zbd	A	29	209	9.6e-58			63.61	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	COMPLEX (GTP-BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-BINDING/EFFECTOR), G PROTEIN, EFFECTOR, RABCD, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN
1323	2nrg	A	33	230	1.6e-46			57.05	GTP BINDING PROTEIN (G25K); CHAIN: A; GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B;	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3, HYDROLASE
1323	3rab	A	30	204	1.6e-58			67.16	RAB3A; CHAIN: A;	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE
1324	1a6o		167	536	1.6e-80			107.93	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1324	1aq1		196	503	0			129.21	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	SER/THR KINASE PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION
1324	1bi8	A	197	493	1.6e-81			122.05	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1324	1bx	A	192	499	3.2e-91			133.50	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1324	1cmk	E	160	503	8e-48			102.25	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1324	1ctp	E	165	503	3.2e-47			102.19	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	
1324	1hcl		196	503	0			141.09		PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1324	1ian		180	567	1.6e-97			117.40	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1324	1jnk		180	563	9.6e-100			136.35	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1324	1kob	A	170	522	1.6e-51			105.97	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1324	1p38		179	570	0			150.88	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1324	1pme		190	568	0			128.64	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1324	3erk		181	509	0			140.27	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1325	1a60		167	496	6.4e-80			108.11	PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1325	1aq1		196	503	0			129.37	CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1325	1bi8	A	197	493	8e-86			122.26	CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1325	1bi9	A	192	499	1.3e-94			133.76	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1325	1cmk	E	160	503	3.2e-49			102.41	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	
1325	1ctp	E	165	503	3.2e-49			102.34	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP-DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	
1325	1hcl		196	503	0			141.19	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1325	1ian		180	567	0			118.03	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1325	1jnk		180	563	4.8e-100			136.46	C-JUN N-TERMINAL KINASE;	TRANSFERASE JNK3;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: NULL;	TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1325	1kob	A	170	522	9.6e-53			106.60	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1325	1p38		179	570	0			151.09	MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1325	1pme		190	568	0			128.85	ERK2; CHAIN: NULL;	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1325	1tki	A	194	519	1.1e-44			99.53	TITIN; CHAIN: A, B;	SERINE KINASE SERINE KINASE, TITIN, MUSCLE, AUTOINHIBITION
1325	3erk		181	509	0			140.42	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1327	1cs8	A	1	350	0			368.72	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1328	1cs8	A	19	391	0			412.39	HUMAN PROCATHEPSIN L; CHAIN: A;	HYDROLASE PROSEGMENT, PROPEPTIDE, INHIBITION, HYDROLASE
1333	1edh	A	65	269	8e-50			124.30	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1333	1ncj	A	64	268	8e-52			129.50	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1335	1adl		3	133	9.6e-56			158.94	LIPID-BINDING PROTEIN ADIPOCYTE LIPID-BINDING PROTEIN COMPLEXED WITH ARACHIDONIC 1ADL 3 ACID 1ADL 4	
1335	1hmr		3	133	6.4e-58			146.24	LIPID-BINDING PROTEIN FATTY ACID BINDING PROTEIN (HUMAN MUSCLE, M-FABP) COMPLEXED 1HMR 3 WITH ONE MOLECULE OF ELAIDIC ACID 1HMR 4	
1335	1pmp	A	3	133	3.2e-55			161.49	CELLULAR LIPOPHILIC TRANSPORT PROTEIN P2 MYELIN PROTEIN (P2) 1PMP 3	
1340	1a12	A	11	409	1.6e-78			141.30	REGULATOR OF CHROMOSOME CONDENSATION I; CHAIN: A, B, C;	GUANINE NUCLEOTIDE EXCHANGE FACTOR RCC1; GUANINE NUCLEOTIDE EXCHANGE FACTOR, GEF, RAN, 2 RAS-LIKE NUCLEAR GTP BINDING PROTEIN HEADER TER
1345	1a45		1	148	1.4e-61			122.87	GAMMA F CRYSTALLIN; CHAIN: NULL	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1a5d	A	1	148	4.8e-63			121.88	GAMMA E CRYSTALLIN; CHAIN: A, B	EYE LENS PROTEIN EYE LENS PROTEIN
1345	1am m		1	148	3.2e-65			125.68	GAMMA B-CRYSTALLIN; CHAIN: NULL;	CRYSTALLIN GAMMA II- CRYSTALLIN EYE LENS PROTEIN, CRYSTALLIN
1345	1bd7	A	1	147	1.6e-39			80.96	CIRCULARLY PERMUTED BB2-CRYSTALLIN; CHAIN: A, B;	EYE-LENS PROTEIN EYE-LENS PROTEIN, BETA-CRYSTALLIN B,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1345	1elp	A	1	148	1.3e-62			122.84	GAMMA-D CRYSTALLIN; CHAIN: A, B	EYE-LENS PROTEIN, 2 MULTIGENE FAMILY EYE LENS PROTEIN EYE LENS PROTEIN
1345	1got	B	48	388	9.6e-31			60.77	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT-BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	COMPLEX (GTP-BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMA1, TRANSDUCIN GAMMA SUBUNIT; COMPLEX (GTP-BINDING/TRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION
1345	2bb2		1	148	1.6e-47			99.58	EYE LENS PROTEIN BETA-B2-CRYSTALLIN 2BB2 3	
1352	2fha		6	177	8e-73			273.99	FERRITIN; CHAIN: NULL;	IRON STORAGE IRON STORAGE
1353	iqub	A	184	484	1.6e-11			84.05	HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1363	lawc	B	38	192	1.6e-39			64.05	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABP ALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1363	1bd8		2	161	8e-30			54.79	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1363	1blx	B	1	165	8e-29			55.34	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR KINASE, CYCLIN-DEPENDENT ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1363	1bu9	A	31	212	1.6e-34			54.53	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1363	1ihb	A	5	162	8e-34			54.88	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1363	likn	D	73	307	4.8e-38			67.03	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1363	1myo		39	156	3.2e-25			53.66	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLLATION, NMR, ANK-REPEAT
1363	1nfi	E	31	243	1.6e-38			64.27	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1366	1dqv	A	143	415	8.5e-91	0.64	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SAND WICH, CALCIUM ION, C2 DOMAIN
1366	1dqv	A	144	415	3.2e-46	0.49	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SAND WICH, CALCIUM ION, C2 DOMAIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1366	lrsy		134	270	3.4e-40	0.40	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1366	lrsy		134	270	3.4e-40			122.64	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN 1 (FIRST C2 DOMAIN) (CALB) IRSY 3	
1368	lbu7	A	42	505	1.6e-92			197.06	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1368	loxa		23	504	3.2e-31			67.59	CYTOCHROME P450 ERYF; 10XA 5 CHAIN: NULL 10XA 6	OXIDOREDUCTASE (OXYGENASE)
1372	lbg2		2	340	8e-89			210.20	KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1372	lbg2		4	340	8e-89	0.54	1.00		KINESIN; CHAIN: NULL;	MOTOR PROTEIN MOTOR PROTEIN, ATPASE, MICROTUBULE ASSOCIATED
1372	lcz7	A	1	340	6.8e-79	0.65	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	lcz7	A	1	341	3.2e-72	0.46	1.00		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1372	1cz7	A	1	342	6.8e-79			156.19	MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1372	2kin	A	2	252	1.2e-58			139.58	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	A	4	252	3.2e-57	0.25	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	A	6	252	1.2e-58	0.29	1.00		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	B	265	352	3.4e-28	-0.01	0.98		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2kin	B	265	358	8e-27	-0.02	0.99		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	2ncd	A	1	339	1.6e-72	0.46	1.00		KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	2ncd	A	1	340	1.6e-72			152.53	KINESIN MOTOR NCD; CHAIN: A;	CONTRACTILE PROTEIN KINESIN, MICROTUBULE-BASED MOTOR, NCD, CONTRACTILE PROTEIN
1372	3kar		5	338	5.1e-74			185.05	KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1372	3kar		6	339	6.4e-72	0.31	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1372	3kar	•	7	338	5.1e-74	0.50	1.00		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1372	3kin	B	269	352	1.4e-26	0.19	0.99		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1372	3kin	B	269	384	3.2e-26	-0.10	0.98		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1373	1a4y	A	123	448	4.8e-12	0.19	0.04		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	134	545	4.8e-09	0.26	-0.05		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	45	361	9.6e-14	0.10	0.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1373	1a4y	A	63	230	1e-19	0.29	0.37		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1373	1a9n	A	114	264	5.1e-19	0.66	0.42		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	3 REPEATS COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	A	65	220	3.4e-22	0.43	0.17		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	A	90	231	3.4e-19	0.55	0.65		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	114	264	3.4e-18	0.48	0.53		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	65	220	1.4e-22	0.24	0.04		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1a9n	C	90	231	3.4e-19	0.66	0.55		U2 RNA HAIRPIN IV; CHAIN: Q; R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1373	1bih	A	294	387	6.8e-14	0.33	0.77		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1373	1bih	A	295	427	1.7e-10	0.37	0.25		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1373	1bpv		421	506	3.4e-07	-0.04	0.07		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1373	1cs6	A	286	388	8.5e-15	0.01	-0.05		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1cs6	A	295	409	3.4e-12	0.31	0.19		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1373	1cvs	C	306	389	8.5e-14	0.65	1.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1373	1cvs	D	296	383	1.2e-14	0.29	0.57		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1373	1d0b	A	152	310	6.4e-26	0.02	0.05		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	176	332	8e-24	0.09	-0.15		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	37	211	1.4e-22	0.13	0.57		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	423	547	1.6e-14	0.05	-0.19		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1d0b	A	79	265	8e-22	0.31	0.30		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1373	1dce	A	32	95	9.6e-09	-0.43	0.23		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1dce	A	37	171	8e-08	-0.03	0.15		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 Å 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1373	1ds9	A	56	186	1.6e-10	-0.41	0.28		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1373	1ev2	E	292	383	5.1e-14	0.13	-0.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1373	1ev2	G	296	387	6.8e-16	0.22	0.13		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1373	1fqv	A	64	231	1.7e-13	0.26	0.54		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1373	1fs2	A	53	231	3.4e-18	0.03	0.31		SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN A/CDK2-

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQPOL D score	Compound	PDB annotation
									CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1373	1hnf		303	405	1.7e-08	0.39	0.27		T LYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (HUMAN) I HNF 3	
1373	1nct		292	383	6.8e-19	0.56	0.31		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1373	1tnm		305	383	1.7e-16	0.60	0.76		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1373	1ttf		424	502	3.4e-07	-0.29	0.40		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) I TTF 3 (NMR, 36 STRUCTURES)	
1373	1vca	A	297	394	1.7e-11	0.46	0.16		HUMAN VASCULAR CELL ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	CELL ADHESION PROTEIN VCAM-D1.2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15
1373	1wio	A	280	411	3.4e-12	0.37	0.00		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1373	1yrg	A	132	362	1.1e-09	0.04	-0.14		GTPASE-ACTIVATING PROTEIN RNA1 SCHPO;	TRANSCRIPTION RNAIP; RANGAP; GTPASE-ACTIVATING PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, B;	FOR SPII, GTPASE-ACTIVATING PROTEIN; GAP, RNAIP, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1373	2bnh		45	359	1.4e-18	0.04	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2bnh		47	231	1.7e-23	0.13	0.06		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1373	2dli	A	294	396	3.4e-11	0.20	-0.05		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1373	3ncm	A	296	383	3.4e-17	0.92	0.35		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1374	1cun	A	65	293	0.0017			61.31	ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1374	1cz7	A	1	131	5.1e-34	-0.46	0.66		MICROTUBULE MOTOR PROTEIN NCD; CHAIN: A, B, C, D;	CONTRACTILE PROTEIN NCD, CLARET SEGREGATIONAL PROTEIN; NCD CRYSTAL STRUCTURE, MICROTUBULE MOTORS, KINESIN 2 SUPERFAMILY, CONTRACTILE PROTEIN
1374	1quu	A	53	295	3.4e-05			66.44	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1374	1sig		36	318	0.0017			65.31	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1374	2kin	A	1	42	5.1e-15	-0.55	0.12		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	141	1.7e-27	-0.41	0.81		KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	2kin	B	55	154	1.7e-27			65.43	KINESIN; CHAIN: A, B;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kar		1	127	1e-30	-0.52	0.60		KINESIN-LIKE PROTEIN KAR3; CHAIN: NULL;	CONTRACTILE PROTEIN CONTRACTILE PROTEIN, KAR3, KINESIN-RELATED PROTEIN, MOTOR 2 PROTEIN, ATPASE, P-LOOP, MICROTUBULE BINDING PROTEIN
1374	3kin	B	59	142	6.8e-25	-0.15	0.86		KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1374	3kin	B	59	176	6.8e-25			68.48	KINESIN HEAVY CHAIN; CHAIN: A, B, C, D;	MOTOR PROTEIN MOTOR PROTEIN, CYTOSKELETON
1376	1cej	A	323	405	5.1e-19	-0.02	0.03		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1cej	A	364	435	6.8e-17	-0.11	0.41		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	403	481	5.1e-09	0.08	-0.14		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1cej	A	45	128	5.1e-21	0.09	0.53		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	SURFACE PROTEIN MEROZOITE SURFACE ANTIGEN 1, MAJOR BLOOD-STAGE EGF-LIKE DOMAIN, EXTRACELLULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT, SURFACE PROTEIN
1376	1d4v	A	631	733	1.4e-08	0.30	-0.13		TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: B; DEATH RECEPTOR 5; CHAIN: A;	APOPTOSIS TRAIL; DR5; LIGAND-RECEPTOR COMPLEX, TRIMERIC JELLY-ROLL, TNF-R 2 SUPERFAMILY, APOPTOSIS
1376	1dqb	A	181	252	5.1e-14	0.76	0.78		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1dqb	A	321	406	5.1e-18	0.30	0.15		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1dqb	A	400	485	5.1e-10	-0.07	0.00		THROMBOMODULIN; CHAIN: A;	ANTICOAGULANT, GLYCOSYLATION
1376	1dqb	A	44	131	5.1e-18	0.25	0.21		THROMBOMODULIN; CHAIN: A;	MEMBRANE PROTEIN NMR, THROMBIN, EGF MODULE, ANTICOAGULANT, GLYCOSYLATION
1376	1edm	B	403	433	3.4e-07	-0.14	0.23		FACTOR IX; CHAIN: B, C;	COAGULATION FACTOR CRYSTAL STRUCTURE, EPIDERMAL GROWTH FACTOR, EGF, 2 CALCIUM-BINDING, EGF-LIKE DOMAIN, STRUCTURE AND FUNCTION, 3 HUMAN FACTOR IX, COAGULATION FACTOR
1376	1f7e	A	403	433	5.1e-07	0.09	0.04		BLOOD COAGULATION FACTOR VII; CHAIN: A;	BLOOD CLOTTING FACTOR VII, BLOOD COAGULATION, EGF-LIKE DOMAIN, BLOOD 2 CLOTTING
1376	1fjs	L	216	254	1.2e-12	0.66	0.23		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	284	335	3.4e-20	0.27	0.42		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	327	374	1.7e-17	-0.13	0.25		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	407	445	1.4e-15	0.08	0.94		COAGULATION FACTOR XA; CHAIN: A; COAGULATION	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FACTOR XA; CHAIN: L;	COAGULATION COFACTOR, PROTEASE
1376	1fjs	L	49	90	1.7e-12	0.83	0.59		COAGULATION FACTOR XA; CHAIN: A; COAGULATION FACTOR XA; CHAIN: L;	BLOOD CLOTTING PROTEIN INHIBITOR COMPLEX, COAGULATION COFACTOR, PROTEASE
1376	1hcg	B	217	254	3.4e-12	0.50	0.46		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1hcg	B	286	334	1.2e-18	0.34	0.33		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1hcg	B	407	445	8.5e-15	0.45	0.89		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1hcg	B	49	90	5.1e-12	0.45	0.95		COAGULATION FACTOR BLOOD COAGULATION FACTOR XA IHCG 3	
1376	1kig	L	327	374	3.4e-18	0.01	0.31		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1kig	L	407	445	6.8e-15	-0.06	0.82		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1kig	L	49	90	5.1e-12	0.66	0.34		FACTOR XA; CHAIN: H, L; ANTICOAGULANT PEPTIDE; CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) RTAP; GLYCOPROTEIN, SERINE PROTEASE, PLASMA, BLOOD COAGULATION, 2 COMPLEX (PROTEASE/INHIBITOR)
1376	1kdo		135	322	6.8e-14	0.47	-0.11		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1klo		286	433	1.7e-20	0.16	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1klo		626	787	8.5e-10	0.38	0.00		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1376	1pfx	L	121	254	1.7e-14	0.04	0.01		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1pfx	L	289	427	3.4e-27	0.02	0.23		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1pfx	L	41	152	8.5e-26	0.21	0.89		FACTOR IXA; CHAIN: C, L, D; PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1376	1qfk	L	131	226	1.4e-22	0.28	0.37		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	177	252	8.5e-16	0.18	0.72		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	PROTEASE
1376	1qfk	L	286	389	3.4e-26	-0.11	0.22		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	326	419	1.5e-21	-0.01	0.29		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	367	445	1e-18	0.22	0.99		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	48	141	1.7e-24	0.12	0.92		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1376	1qfk	L	89	189	6.8e-23	-0.29	0.52		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1qub	A	41	444	1.7e-46	0.02	-0.18		HUMAN BETA2-GLYCOPROTEIN I; CHAIN: A;	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI, COMPLEMENT CONTROL PROTEIN, 2 N-GLYCOSYLATION, MULTI-DOMAIN, MEMBRANE ADHESION
1376	1rfn	B	175	228	1e-13	0.24	0.35		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	285	339	3.4e-19	0.29	-0.01		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	407	445	3.4e-11	0.13	0.94		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1rfn	B	49	102	8.5e-12	0.67	-0.15		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1376	1sfp		805	918	3.4e-21	0.64	0.48		ASFP; CHAIN: NULL;	SPERMADHESIN ACIDIC SEMINAL PROTEIN; SPERMADHESIN, BOVINE SEMINAL PLASMA PROTEIN, ACIDIC 2 SEMINAL FLUID PROTEIN, ASFP, CUB DOMAIN, X-RAY CRYSTAL 3 STRUCTURE, GROWTH FACTOR
1376	1spp	B	809	922	3.4e-22	0.37	0.65		MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-I; CHAIN: A; MAJOR SEMINAL PLASMA GLYCOPROTEIN PSP-II; CHAIN: B	COMPLEX (SEMINAL PLASMA PROTEIN/SPP) SEMINAL PLASMA PROTEINS, SPERMADHESINS, CUB DOMAIN 2 ARCHITECTURE, COMPLEX (SEMINAL PLASMA PROTEIN/SPP)

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1376	1tpg		68	158	1.5e-21	0.05	0.04		T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PLASMINOGEN ACTIVATION
1376	1xka	L	131	230	1.7e-15	0.09	0.59		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	182	254	1.7e-15	-0.01	0.43		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	286	380	5.1e-20	0.25	0.69		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	367	444	3.4e-19	0.28	0.40		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1376	1xka	L	48	145	3.4e-22	0.01	0.55		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1381	1a06		205	530	5.1e-62	-0.04	0.71		CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE; CHAIN: NULL;	KINASE KINASE, SIGNAL TRANSDUCTION, CALCIUM/CALMODULIN
1381	1a06		236	534	5.1e-62			109.19	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1381	1a6o		194	550	6.8e-40			84.57	CHAIN: NULL; PROTEIN KINASE CK2/ALPHA-SUBUNIT; CHAIN: NULL;	CALCIUM/CALMODULIN TRANSFERASE TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, CASEIN KINASE, 2 SER/THR KINASE
1381	1bi8	A	204	485	5.1e-41	0.21	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A, C; CYCLIN-DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	COMPLEX (KINASE/INHIBITOR) CDK6; P19INK4D; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, COMPLEX (KINASE/INHIBITOR) HEADER HELIX
1381	1blx	A	198	495	1.2e-46			92.79	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1381	1blx	A	199	485	1.2e-46	0.40	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1381	1csn		203	469	6.8e-48	0.06	0.74		CASEIN KINASE-1; ICSN 4	PHOSPHOTRANSFERASE
1381	1ctp	E	169	524	3.4e-71			154.37	TRANSFERASE(PHOSPHOTRANSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATALYTIC SUBUNIT) ICTP 4	
1381	1ctp	E	196	498	3.4e-71	0.41	1.00		TRANSFERASE(PHOSPHOTRANSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1381	1hel		202	495	1.7e-53	0.39	1.00		(CATALYTIC SUBUNIT) ICTP 4 HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	1hel		202	499	1.7e-53			115.78	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1381	lian		183	555	3.4e-40			92.87	P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	lian		203	475	3.4e-40	0.01	0.88		P38 MAP KINASE; CHAIN: NULL;	SERINE/THREONINE-PROTEIN KINASE CSBP, RK, P38; PROTEIN SER/THR-KINASE, SERINE/THREONINE-PROTEIN KINASE
1381	ljnk		185	577	1.7e-46			112.39	C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	ljnk		203	512	1.7e-46	0.21	1.00		C-JUN N-TERMINAL KINASE; CHAIN: NULL;	TRANSFERASE JNK3; TRANSFERASE, JNK3 MAP KINASE, SERINE/THREONINE PROTEIN 2 KINASE
1381	lkob	A	170	570	1.7e-68			127.80	TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1381	lkob	A	205	493	1.7e-68	0.52	1.00		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1381	3erk		198	498	8.5e-53	0.54	1.00		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	INTRASTERIC REGULATION TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1381	3erk		213	562	8.5e-53			98.67	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1384	1ao7	E	52	210	9.6e-54	0.39	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1ao7	E	52	210	9.6e-54			128.38	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66	0.48	1.00		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1384	1bd2	E	52	210	3.2e-66			143.49	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1384	1bec	•	52	210	6.4e-66			130.56	CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E; 14.3.D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN: NULL; IBEC 6	RECEPTOR T CELL RECEPTOR IBEC 14
1384	1bec		53	210	6.4e-66	0.49	1.00		14.3.D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN: NULL; IBEC 6	RECEPTOR T CELL RECEPTOR IBEC 14
1384	1fyt	E	53	210	8e-60	0.25	1.00		HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HAI PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DRI, DRA; HLA-DRI, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
1384	1tcr	B	50	210	9.6e-64	0.43	1.00		ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1384	1tcr	B	51	210	9.6e-64			131.76	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	RECEPTOR TCR; T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL
1388	1a4y	A	21	309	3.2e-17	0.04	-0.11		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPTOPE MAPPING, LEUCINE-RICH 3 REPEATS
1388	1a9n	A	26	156	3.4e-21	0.43	-0.01		U2 RNA HAIRPIN IV; CHAIN: Q;	COMPLEX (NUCLEAR

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	A	46	155	4.8e-06	0.28	0.19		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	A	4	121	1.5e-20	0.48	0.65		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	24	106	1.3e-05	0.51	0.51		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	26	156	1.2e-21	0.41	-0.08		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	46	155	4.8e-06	0.42	0.06		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1a9n	C	4	121	6.8e-20	0.67	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN
1388	1cs6	A	77	280	0.00034	-0.15	0.07		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1388	1d0b	A	19	194	6.4e-27	0.50	0.77		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1d0b	A	4	128	1.4e-12	0.27	0.89		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1388	1d0b	A	63	216	1.4e-25	0.28	0.43		INTERNALIN B; CHAIN: A;	ADHESION CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1d0b	A	87	236	3.2e-25	-0.05	0.04		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1388	1dce	A	21	127	3.2e-11	0.27	0.90		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1dce	A	46	170	1.6e-12	0.59	0.96		RAB GERANYLGERANYLTRANSFERASE RASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE RASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1388	1ds9	A	103	236	6.4e-13	0.08	-0.02		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1388	1fo1	A	41	103	3.2e-06	-0.05	0.40		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1fo1	A	89	171	4.8e-07	-0.06	0.10		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1fo1	B	41	103	3.2e-06	0.26	0.04		NUCLEAR RNA EXPORT	RNA BINDING PROTEIN TAP (NFX1);

SEQ ID NO.	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									FACTOR 1; CHAIN: A, B;	RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1388	1fqv	A	1	173	1.4e-09	0.29	-0.08		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N; P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fqv	A	20	213	1.6e-14	0.12	0.10		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N; P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fqv	A	22	298	4.8e-11	0.08	-0.15		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N; P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1388	1fs2	A	11	128	3.4e-12	0.21	0.09		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	1fs2	A	20	213	1.6e-14	0.04	0.03		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1388	2bth		5	131	1.7e-19	0.07	-0.12		RIBONUCLEASE INHIBITOR;	ACETYLATION RNASE INHIBITOR,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1388	2bnh		74	439	3.2e-20	0.06	-0.15		CHAIN: NULL; RIBONUCLEASE INHIBITOR; CHAIN: NULL;	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1389	1klo		476	643	1.6e-13	0.05	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1392	1aj4		10	114	3.2e-23	-0.36	0.01		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
1392	1ak8		2	61	3.2e-22	0.21	0.48		CALMODULIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN CALMODULIN C ₁ -RICH- DOMAIN, RESIDUES 1 - 75; CERIUM-LOADED, CALCIUM-BINDING PROTEIN
1392	1cdm	A	2	117	4.8e-33	-0.32	0.16		CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF 1CDM 3 CALMODULIN-DEPENDENT PROTEIN KINASE II 1CDM 4	
1392	1cll		1	132	3.2e-38			53.74	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL.3	
1392	1cll		2	117	3.2e-38	-0.37	0.11		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL.3	
1392	1dlf	A	10	117	1.6e-21	-0.54	0.12		CARDIAC TROPONIN C; CHAIN: A;	STRUCTURAL PROTEIN HELIX-TURN-HELIX
1392	1exr	A	2	117	1.6e-35	-0.22	0.23		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1392	1tcf		1	139	3.2e-28			56.30	TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION, REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1392	1tcf		2	111	3.2e-28	-0.35	0.11		TROPONIN C; CHAIN: NULL;	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION, REGULATORY DOMAIN, CALCIUM-REGULATED 3 MUSCLE CONTRACTION
1392	1tnx		2	111	8e-24	-0.32	0.33		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	CALCIUM-BINDING PROTEIN EF-HAND 1TNX 14
1392	1top		1	141	4.8e-28			51.47	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1392	1top		2	111	4.8e-28	-0.03	0.36		CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	
1392	1vrk	A	1	135	1.4e-37			51.68	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1392	1vrk	A	2	117	1.4e-37	-0.42	0.27		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1396	1b0x	A	934	1000	1.7e-24	1.07	1.00		EPHA4 RECEPTOR TYROSINE KINASE; CHAIN: A;	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										DIMERIZATION DOMAIN, TRANSFERASE
1396	1b4f	A	934	999	8.5e-27	0.92	1.00		EPHB2; CHAIN: A, B, C, D, E, F, G, H;	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER RECEPTOR RECEPTOR, SIGNAL TRANSDUCER OF IL-6 TYPE
1396	1b58		431	537	7.5e-22	0.26	0.46		GP130; CHAIN: NULL;	CYTOKINES, THIRD 2 N-TERMINAL DOMAIN, TRANSMEMBRANE, GLYCOPROTEIN
1396	1bp3	B	328	531	1.5e-25	-0.06	0.01		GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B;	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR
1396	1bpv		438	536	4.5e-18	0.20	0.60		TITIN; CHAIN: NULL;	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III
1396	1byg	A	627	899	3e-93			169.44	C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2
1396	1byg	A	628	897	1.4e-90	0.83	1.00		C-TERMINAL SRC KINASE; CHAIN: A;	STAUSPORINE, TRANSFERASE
1396	1byg	A	629	898	3e-93	0.64	1.00		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2
1396	1c8p	A	437	531	6e-19	0.46	1.00		CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	STAUSPORINE, TRANSFERASE
1396	1cd9	B	328	524	4.5e-35	0.40	0.07		GRANULOCYTE COLONY-STIMULATING FACTOR; CHAIN: A, C; G-CSF RECEPTOR;	MEMBRANE, PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN
										CYTOKINE G-CSF; G-CSF-R; CLASS I CYTOKINE, HEMATOPOIETIC RECEPTOR, SIGNAL

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1396	1cto		454	531	6e-19	0.32	0.63		CHAIN: B, D; GRANULOCYTE COLONY-STIMULATING FACTOR RECEPTOR; CHAIN: NULL;	TRANSDUCTION BINDING PROTEIN BINDING PROTEIN, CYTOKINE RECEPTOR
1396	1em	A	338	531	4.5e-22	-0.12	0.28		ERYTHROPOIETIN RECEPTOR; CHAIN: A, B;	CYTOKINE EBF; ERYTHROPOIETIN RECEPTOR, SIGNAL TRANSDUCTION, CYTOKINE 2 RECEPTOR CLASS 1
1396	1f6f	C	408	531	4.5e-13	-0.05	0.15		PLACENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	HORMONE/GROWTH FACTOR/HORMONE RECEPTOR 4-HELICAL BUNDLE, ALPHA HELICAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CYTOKINE-RECEPTOR COMPLEX
1396	1fgk	A	617	900	0			179.56	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1396	1fgk	A	621	895	0	0.91	1.00		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1396	1fgk	B	614	899	0			182.22	FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1396	1fgk	B	620	895	0	0.87	1.00		FGF RECEPTOR 1; CHAIN: A, B;	RECEPTOR, PHOSPHOTRANSFERASE
1396	1fmk		615	903	0	0.88	1.00		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1396	1fna		454	524	1.2e-13	0.39	0.63		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 1FNA 3	
1396	1fnf		322	531	3e-26	0.08	-0.05		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1396	1fpu	A	623	897	0	0.71	1.00		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1396	1ir3	A	623	910	0			188.00	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE, TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE))
1396	1ir3	A	626	910	0	0.81	1.00		INSULIN RECEPTOR; CHAIN: A;	COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									PEPTIDE SUBSTRATE; CHAIN: B;	(TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1396	1mfn		331	533	1.3e-25	0.08	0.53		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN
1396	1nuk	A	31	202	1.5e-83	0.58	1.00		TYROSINE-PROTEIN KINASE RECEPTOR EPH; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPH RECEPTOR TYROSINE KINASE,
1396	1nuk	A	31	202	1.5e-83			182.17	TYROSINE-PROTEIN KINASE RECEPTOR EPH; CHAIN: A;	TRANSFERASE NUK; TRANSFERASE, EPH RECEPTOR TYROSINE KINASE,
1396	1qcf	A	610	902	0	0.90	1.00		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1396	1qg3	A	329	534	1.5e-36	0.19	0.22		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qg3	A	331	522	6.8e-11	0.03	0.18		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1396	1qpc	A	621	900	0	0.97	1.00		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1396	1qr4	A	331	529	1.5e-30	0.27	-0.03		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1396	1sgg		934	995	1.7e-25	1.03	1.00		EPHRII TYPE-B RECEPTOR 2; CHAIN: NULL;	EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1396	1tff		440	524	1e-17	0.13	0.25		GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3	TYROSINE-PROTEIN KINASE NMR, RECEPTOR OLIGOMERIZATION, EPH RECEPTORS, TYROSINE 2, PHOSPHORYLATION, SIGNAL TRANSDUCTION, TYROSINE-PROTEIN 3 KINASE
1396	1vr2	A	622	897	5.1e-98	0.88	1.00		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TRANSFERASE KDR; TYROSINE KINASE
1396	2fnb	A	326	423	3e-09	0.07	-0.14		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1396	2fnb	A	439	529	9e-19	0.36	0.17		FIBRONECTIN; CHAIN: A;	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING
1396	2hft		324	524	6e-34	0.22	-0.18		HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	COAGULATION FACTOR
1401	1akh	A	81	121	6e-05	1.11	0.99		MATING-TYPE PROTEIN A-1; CHAIN: A; MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;	COMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA-BINDING PROTEIN, DNA, TRANSCRIPTION REGULATION
1401	1au7	A	83	125	0.00015	0.82	0.94		PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) GHF-1; COMPLEX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										(DNA-BINDING PROTEIN/DNA), PITUITARY, CPD, 2 POU DOMAIN, TRANSCRIPTION FACTOR
1401	1b72	B	83	125	0.0006	0.27	0.43		HOMEBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E; INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA
1401	1bw5		83	125	6e-05	0.73	0.93			DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN
1401	1du6	A	83	127	0.0003	-0.11	0.03		HOMEBOX PROTEIN PBX1; CHAIN: A;	GENE REGULATION PBX1; HOMEODOMAIN
1401	1fjl	B	83	125	0.0003	0.82	0.99		PAIRED PROTEIN; CHAIN: A, B; C; DNA; CHAIN: D, E, F	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION
1401	1hdp		83	125	0.00015	0.50	0.80		DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) IHDP	
1401	1mnm	C	82	125	0.00015	0.63	1.00		MCM1 TRANSCRIPTIONAL REGULATOR; CHAIN: A, B; MAT ALPHA-2 TRANSCRIPTIONAL REPRESSOR; CHAIN: C, D; STE6 OPERATOR DNA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION/HOMEBOX/DNA) PHEROMONE RECEPTOR; TRANSCRIPTION FACTOR; MATING-TYPE PROTEIN ALPHA-2; TRANSCRIPTION REGULATION, TRANSCRIPTIONAL REPRESSION, 2 DNA-BINDING PROTEIN, COMPLEX (TRANSCRIPTION/HOMEBOX/DNA)
1401	1ocp		83	125	9e-06	0.28	0.84		OCT-3; 1OCP 5 CHAIN: NULL; 1OCP 6	DNA-BINDING PROTEIN
1401	1pog		83	125	0.0001	0.41	0.96		DNA BINDING PROTEIN OCT-1 POU HOMEODOMAIN DNA-BINDING PROTEIN MUTANT	

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									WITH IPOG 3 ARG GLY SER HIS MET INSERTED AT THE N-TERMINUS AND ASP ILE IPOG 4 INSERTED AT THE C-TERMINUS (INSRGSHM-R6),INS(166-DI) IPOG 5 (NMR, 13 STRUCTURES) IPOG 6	
1403	1a36	A	644	772	5.1e-08	0.03	-0.09		TOPOISOMERASE I; CHAIN: A; DNA; CHAIN: B, C;	COMPLEX (ISOMERASE/DNA) COMPLEX (ISOMERASE/DNA), DNA, TOPOISOMERASE I
1403	1dn1	B	389	556	0.00017	-0.16	0.00		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1403	1or3	A	527	634	0.00017	-0.13	0.19		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APOE3; LIPID TRANSPORT, HEPARIN-BINDING, PLASMA PROTEIN, HDL, VLDL
1403	1quu	A	367	551	6e-15	-0.12	0.04		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1404	1c28	A	826	947	1e-27	1.14	0.39		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	B	827	947	6e-22	0.71	-0.13		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1c28	C	826	947	4.5e-18	0.84	0.43		30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN CHAIN: A, B, C;	SERUM PROTEIN ACRP30 C1Q TNF TRIMER ALL-BETA, SERUM PROTEIN
1404	1cun	A	375	591	6e-12	-0.03	0.29		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1404	1cum	A	436	651	4.5e-07	0.02	0.03		ALPHA SPECTRIN; CHAIN: A, B, C;	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1404	1fio	A	292	467	6e-07	-0.08	0.19		SSO1 PROTEIN; CHAIN: A;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1404	1hae		120	150	0.0045	0.07	0.11		HERGULIN-ALPHA; CHAIN: NULL;	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX
1404	1hre		120	150	0.0045	0.13	0.25		GROWTH FACTOR HERGULIN-ALPHA (EPIDERMAL GROWTH FACTOR-LIKE DOMAIN) 1HRE 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1HRE 4	GROWTH FACTOR NEU DIFFERENTIATION FACTOR (RAT), ACETYLCHOLINE GROWTH FACTOR
1407	1b6c	B	25	129	1.4e-09	-0.26	0.12		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1407	1fgk	A	22	126	1.7e-05	-0.02	0.04		FGF RECEPTOR I; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR I; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1407	1fmk		22	127	3e-05	0.17	0.36		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1407	1fpu	A	22	130	1.5e-05	-0.09	0.18		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B; ERK2; CHAIN: NULL;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1407	1pme		21	131	7.5e-06	-0.12	0.37			TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSFERASE
1407	1qcf	A	22	129	9e-05	-0.56	0.11		HAEMATOPHOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1407	1qpc	A	22	61	7.5e-05	-0.75	0.23		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1407	3erk		21	126	1.5e-05	-0.35	0.09		EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERINE/THREONINE-PROTEIN KINASE, MAP KINASE, 2 ERK2
1408	1a44		2	168	4.5e-70	0.60	1.00		PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1a44		2	168	4.5e-70			267.15	PHOSPHATIDYLETHANOLAMI NE-BINDING PROTEIN; CHAIN: NULL;	LIPID-BINDING PROTEIN PEBP, PBP LIPID-BINDING
1408	1beh	A	3	168	3e-68	0.89	1.00		PHOSPHATIDYLETHANOLAMI NE BINDING PROTEIN; CHAIN: A, B;	LIPID-BINDING LIPID-BINDING, SIGNALLING
1408	1beh	A	3	168	3e-68			271.38	PHOSPHATIDYLETHANOLAMI NE BINDING PROTEIN; CHAIN:	LIPID-BINDING LIPID-BINDING, SIGNALLING

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A, B;	
1410	1a88	A	47	319	0.00015	0.25	0.90		CHLOROPEROXIDASE L; CHAIN: A, B, C;	HALOPEROXIDASE BROMOPEROXIDASE L; HALOPEROXIDASE L; HALOPEROXIDASE; OXIDOREDUCTASE
1410	1a8s		47	319	9e-08	0.13	0.45		CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE HALOPEROXIDASE F; HALOPEROXIDASE; OXIDOREDUCTASE, PROPIONATE COMPLEX
1410	1azw	A	11	319	4.5e-05			60.20	PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1azw	A	47	319	4.5e-05	0.00	0.42		PROLINE IMINOPEPTIDASE; CHAIN: A, B;	AMINOPEPTIDASE AMINOPEPTIDASE, PROLINE IMINOPEPTIDASE, SERINE PROTEASE, 2 XANTHOMONAS CAMPESTRIS
1410	1b6g		12	325	1.5e-08			61.14	HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1b6g		35	318	1.5e-08	0.13	0.77		HALOALKANE DEHALOGENASE; CHAIN: NULL;	HYDROLASE HYDROLASE, HALOALKANE DEHALOGENASE, ALPHA/BETA-HYDROLASE
1410	1cqW	A	10	319	6e-09	0.38	0.99		HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND
1410	1cv2	A	47	154	3e-05	-0.16	0.19		HALOALKANE DEHALOGENASE; CHAIN: A;	HYDROLASE LINB, 1,3,4,6- TETRACHLORO-1,4- CYCLOHEXADIENE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1410	1ek1	A	47	321	1.1e-07	0.12	0.98			DEHALOGENASE, LINDANE, BIODEGRADATION, ALPHA/BETA-HYDROLASE
1410	1ek1	B	47	321	3e-07	0.14	0.95		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	1hlg	A	47	165	0.003	-0.15	0.41		EPOXIDE HYDROLASE; CHAIN: A, B;	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
1410	1qge	D	47	195	0.0006	-0.13	0.10		LIPASE, GASTRIC; CHAIN: A, B; TRIACYLGLYCEROL	HYDROLASE
									HYDROLASE; CHAIN: D; TRIACYLGLYCEROL	PSEUDOMONADACEAE, CIS-PEPTIDE, CLOSED CONFORMATION, 2 HYDROLASE, LID
1410	1qj4	A	47	316	9e-09	0.02	0.37		HYDROXYNITRILE LYASE; CHAIN: A;	LYASE OXYNITRILE LYASE; OXYNITRILASE, CYANOGENESIS, CYANHYDRIN FORMATION, LYASE
1410	1qtr	A	11	321	1.2e-05			57.92	PROLYL AMINOPEPTIDASE; CHAIN: A;	HYDROLASE ALPHA BETA
1410	1qtr	A	74	319	1.2e-05	-0.51	0.12		PROLYL AMINOPEPTIDASE; CHAIN: A;	PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
1410	4lip	D	47	155	9e-05	0.06	0.05		TRIACYL-GLYCEROL-HYDROLASE; CHAIN: D, E;	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMINOPEPTIDASE
										LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE ANALOGUE, ENANTIOSELECTIVITY
1415	1dn1	B	384	513	0.00045	-0.02	0.09		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B;	COMPLEX, MULTI-SUBUNIT
1418	1alh	A	401	426	0.00015	0.11	0.01		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	1alh	A	404	485	3e-24	0.05	0.95		QGSZ ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1418	lmev	C	403	486	4.5e-25			76.20	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lmev	C	404	485	4.5e-25	-0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lmev	C	432	543	6e-23	-0.01	0.53		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lmev	C	461	575	1.2e-21	-0.31	0.06		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1418	lsp1		522	547	1.2e-06	-0.44	0.25		SP1F3; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
1418	lubb	C	408	543	1.4e-24	-0.01	0.07		YY1; CHAIN: C; ADENO-	COMPLEX (TRANSCRIPTION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1418	1ubd	C	432	575	1e-24	-0.42	0.03		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1418	2adr		461	549	4.5e-14	0.04	0.17		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION
1418	2adr		522	575	1.4e-12	-0.41	0.03		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1418	2drp	A	522	577	1.2e-14	-0.69	0.06		COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1418	2gli	A	369	485	3e-20	-0.05	0.47		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1418	2gli	A	404	575	4.5e-33	-0.16	0.25		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
										BINDING PROTEIN(DNA)
1419	1aut	L	118	259	3e-15	0.04	0.17		ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE (PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1419	1dan	L	136	270	1.5e-15			57.15	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEINASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEINASE/COFACTOR/LIGAND)
1419	1dx5	I	136	232	1e-17	0.14	0.24		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN; TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1419	1dx5	I	168	264	1.1e-13	0.33	0.55		THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; FETOMODULIN; TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1419	1ext	A	31	191	3e-16	0.14	-0.11		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	ANTIFIBRINOLYTIC COMPLEX SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1419	1ext	A	61	243	3e-16			59.06	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	PROTEIN SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN
1419	1kdo		125	298	9e-22	0.05	-0.01		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		29	185	4.5e-26	0.54	-0.01		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		61	247	4.5e-27	0.51	0.23		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1klo		77	234	4.5e-27			78.19	LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1419	1pfx	L	13	128	1.1e-25	0.07	-0.09		FACTOR IXA; CHAIN: C, L,; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pfx	L	205	298	6e-21	-0.04	0.18		FACTOR IXA; CHAIN: C, L,; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pfx	L	38	165	6e-30			67.49	FACTOR IXA; CHAIN: C, L,; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pfx	L	76	223	6e-30	-0.30	0.31		FACTOR IXA; CHAIN: C, L,; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR)

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1419	1pp2	R	39	169	1.5e-19	0.24	-0.18		HYDROLASE CALCIUM-FREE PHOSPHOLIPASE A=2= (E.C.3.1.1.4) IPP2 4	
1419	1qfk	L	109	216	3e-15	0.11	0.30		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1419	1qfk	L	145	247	7.5e-15	0.09	-0.06		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1419	1skz		141	271	3e-15	-0.17	0.98		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1419	1skz		66	179	3e-15			55.31	ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1419	1tpg		156	237	4.5e-20	0.31	0.53		T-PLASMINOGEN ACTIVATOR	PLASMINOGEN ACTIVATION

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1419	ltpg		220	297	4.5e-15	-0.31	0.18		F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	
1419	ltpg		29	109	7.5e-19	0.14	-0.01		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1419	lvap	A	145	273	9e-16	0.02	-0.19		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1419	lvap	A	81	236	7.5e-16	0.04	-0.19		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	lvpi		81	204	3e-19	0.07	-0.18		PHOSPHOLIPASE A2	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1419	lxka	L	145	222	9e-14	0.17	0.37		PHOSPHOLIPASE A2 INHIBITOR; CHAIN: NULL	NEUROTOXIN PHOSPHOLIPASE A2 INHIBITOR, X-RAY STRUCTURE, RECOGNITION, 2 MOLECULAR EVOLUTION, NEUROTOXIN
1419	9wga	A	13	142	1.5e-24	0.23	0.30		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1421	lamo	A	272	539	6.8e-40	-0.16	0.01		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	OXIDOREDUCTASE CPR, P450R; X-RAY CRYSTALLOGRAPHY, FLAVOPROTEIN, NITRIC OXIDE SYNTHASE, 2 OXIDOREDUCTASE
1421	lfb3	A	252	538	5.1e-57	-0.13	0.21		NADPH-CYTOCHROME P450 REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE TWO DOMAIN MOTIF, ROSSMANN FOLD

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1421	1fmb		252	538	3.4e-55	0.09	0.01		OXIDOREDUCTASE (NADP+(A), FERREDOXIN(A)) FERREDOXIN:NADP+ OXIDOREDUCTASE (FERREDOXIN REDUCTASE, IFNB 3 FLAVOENZYME) (E.C.1.1.8.1.2) IFNB 4 IFNB 72	
1421	1qfj	A	246	510	3.4e-31	-0.07	0.07		FLAVIN REDUCTASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE RIBOFLAVIN, FLAVIN REDUCTASE, FERREDOXIN REDUCTASE 2 SUPERFAMILY, OXIDOREDUCTASE
1421	1qfz	A	252	537	1.7e-54	-0.14	0.43		FERREDOXIN:NADP+ REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE FNR; FLAVOENZYME, PHOTOSYNTHESIS, ELECTRON TRANSFER, HYDRIDE 2 TRANSFER, OXIDOREDUCTASE
1421	1que		258	538	3.4e-49	0.06	-0.03		FERREDOXIN-NADP+ REDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE FNR; OXIDOREDUCTASE, FLAVOPROTEIN, NADP, FAD, THYLAKOID MEMBRANE, 2 HYCOBILISOME, FNR, NADP+ REDUCTASE
1421	2cnd		244	502	3.4e-57	0.00	-0.12		OXIDOREDUCTASE (NITROGENOUS ACCEPTOR) NADH-DEPENDENT NITRATE REDUCTASE (CYTOCHROME B REDUCTASE 2CND 3 FRAGMENT) (E.C.1.6.6.1) COMPLEXED WITH FAD 2CND 4 (SYNCHROTRON X-RAY DIFFRACTION) 2CND 5	
1426	1alh	A	265	347	1.5e-45			80.07	QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1426	1mey	C	236	318	1e-51			103.77	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C; DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ZINC FINGER, DNA-BINDING PROTEIN COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1426	1tf6	A	236	402	1.7e-38			99.56	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1426	1ubd	C	211	318	6e-54			88.81	YY1; CHAIN: C; ADENOVIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) FIVE-FINGER GLI; PROTEIN/DNA FIVE-FINGER GLI; ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1426	2gli	A	207	347	6e-69			93.51	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)
1434	1bg1	A	191	320	0.00034	0.41	0.27		STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	COMPLEX (TRANSCRIPTION FACTOR/DNA) TRANSCRIPTION FACTOR, PROTEIN-DNA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION FACTOR/DNA)
1434	1bz4	A	187	304	1.7e-05	0.25	0.13		APOLIPOPROTEIN E; CHAIN: A;	LIPID BINDING PROTEIN APO-E3;

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1434	1cui		1	514	1.5e-27			115.08	COLICIN 1A; CHAIN: NULL;	LIPID TRANSPORT, LIPID TRANSPORT, HEPARIN-BINDING, PLASMA 2 PROTEIN, HDL, VLDL REMARK
1434	1cun	A	127	372	7.5e-11	0.07	-0.01		ALPHA SPECTRIN; CHAIN: A, B, C;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1434	1cun	A	228	430	3e-10	0.28	0.00		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	253	475	3e-11	0.10	0.10		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1cun	A	389	494	6e-06	0.40	0.40		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
1434	1dn1	B	296	481	6e-11	0.05	0.18		SYNTAXIN BINDING PROTEIN I; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT
1434	1ez3	A	316	449	1.5e-08	0.18	-0.18		SYNTAXIN-1A; CHAIN: A, B, C;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1434	1ez3	A	364	486	1.5e-08	0.36	-0.02		SYNTAXIN-1A; CHAIN: A, B, C;	BUNDLE ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
1434	1qsa	A	2	514	3e-20			104.88	SOLUBLE LYTIC TRANSGLYCOSYLASE SLT70; CHAIN: A;	TRANSFERASE ALPHA- SUPERHELIX, TRANSFERASE
1434	1quu	A	228	464	1.5e-18	0.21	0.27		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1quu	A	332	481	1.2e-09	0.25	-0.17		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN
1434	1sig		225	512	3e-09			89.88	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1434	1sig		293	514	3e-09	0.14	0.21		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1437	1rgp		1126	1315	1.5e-53			105.03	RHOGAP; CHAIN: NULL;	G-PROTEIN CDC42 GTPASE- ACTIVATING PROTEIN; G-PROTEIN, GAP, SIGNAL-TRANSDUCTION
1437	1tx4	A	1129	1329	4.5e-58			106.55	P50-RHOGAP; CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATING/PROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE), GTPASE, 2 TRANSITION STATE, GAP
1441	1ann		7	299	0			431.20	ANNEXIN IV; IANN 5 CHAIN:	CALCIUM/PHOSPHOLIPID-BINDING

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									NULL; 1ANN 6	PROTEIN 32.5 KDa ENDONEXIN I; 1ANN 7 32.5KD CALECTRIN, ENDOXENIN 1, LIPOCORTIN IV, 1ANN 12 2 CHROMOBINDIN IV, PROTEIN II 1ANN 13
1447	1dhr		9	213	6.8e-55			304.31	Oxidoreductase(acting on NADH or NADPH) dihydropteridine reductase (DHPR) (E.C.1.6.99.10) complex 1DHR 3 WITH NADH 1DHR 4	
1452	1b7f	A	1	151	3.4e-33	0.38	0.54		SXL-lethal protein; chain: A, B; RNA (5'-R(p*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)-chain: P, Q; UP*UP*UP*UP*U)-chain: P, Q;	RNA-BINDING PROTEIN/RNA TRANSCRIPTION PRE-MRNA SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1b7f	A	73	230	6.8e-21	0.38	0.99		SXL-lethal protein; chain: A, B; RNA (5'-R(p*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)-chain: P, Q; UP*UP*UP*UP*U)-chain: P, Q;	RNA-BINDING PROTEIN/RNA TRANSCRIPTION PRE-MRNA SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1b7f	A	73	252	6.8e-21			51.11	SXL-lethal protein; chain: A, B; RNA (5'-R(p*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)-chain: P, Q; UP*UP*UP*UP*U)-chain: P, Q;	RNA-BINDING PROTEIN/RNA TRANSCRIPTION PRE-MRNA SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1452	1cvj	A	1	156	3.4e-46			52.06	Polydenylate binding protein 1; chain: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); chain: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPB 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1cvj	A	5	157	3.4e-46	0.27	0.80		Polydenylate binding protein 1; chain: A, B, C, D.	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPB 1; RRM,

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									E, F, G, H; RNA (5'-R(*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1cvj	A	77	256	5.1e-24	0.02	0.31		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*A)-3') O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPBP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1cvj	B	5	137	6.8e-40	0.25	0.59		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*A)-3')	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPBP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1cvj	B	77	230	1.7e-21	0.08	0.15		O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*A)-3') O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPBP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1cvj	F	77	159	1.7e-19	0.74	1.00		POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*A)-3')	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPBP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1cvj	H	5	130	1.7e-31	-0.03	0.19		O, P, Q, R, S, T; POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*A)-3')	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPBP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

SEQ ID NO:	PDB ID	CHAIN N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1452	1cvj	H	77	159	1.7e-19	0.81	1.00		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PAPBP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1452	1d8z	A	73	153	1.7e-21	0.73	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1452	1ha1		1	151	1.7e-35	0.06	0.07		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	1ha1		75	157	1.7e-21	0.87	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1452	2u2f	A	74	158	3.4e-19			50.59	SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
1452	2up1	A	1	155	1.2e-36	0.28	0.64		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1452	3sxl	A	1	144	3.4e-32	0.13	0.04		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1452	3sxl	A	76	230	1.4e-20	0.20	0.69		SEX-LETHAL; CHAIN: A, B, C;	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1452	3sxl	A	7	146	3.4e-32			53.30	SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1454	1c0t	A	345	668	3.4e-85	-0.04	0.87		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c0t	B	346	668	5.1e-88	-0.17	0.84		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c1c	B •	345	668	0	-0.09	0.99		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON- NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1454	1c9r	A	341	671	1.7e-91	-0.06	0.99		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A);	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT;

cna

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	PsiBlast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P; HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1c9r	B	341	668	8.5e-98	-0.13	0.99		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA
1454	1har		341	551	3.4e-65	0.05	1.00		REVERSE TRANSCRIPTASE HIV-1 REVERSE TRANSCRIPTASE (AMINO-TERMINAL HALF) (FINGERS IHAR 3 AND PALM SUBDOMAINS) (RT216) (E.C.2.7.7.49) IHAR 4	
1454	1mml		326	570	1e-59	0.36	1.00		MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1mml		326	571	1e-59			199.34	MMLV REVERSE TRANSCRIPTASE; 1MML 4 CHAIN: NULL; 1MML 5	REVERSE TRANSCRIPTASE
1454	1rth	A	341	668	0	0.00	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1454	1rth	B	345	668	0	-0.17	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1454	1vrt	A	345	668	0	-0.04	1.00		CHAIN: A, B; 1RTH 5 HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	TRANSCRIPTASE 1RTH 15 NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	1vrt	B	345	668	0	-0.09	1.00		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1454	3hvt	B	342	668	3.4e-100	-0.11	0.66		NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1454	3hvt	B	342	672	3.4e-100			84.10	NUCLEOTIDYLTRANSFERASE REVERSE TRANSCRIPTASE (E.C.2.7.7.49) 3HVT 3	
1455	1dus	A	6	135	5.1e-13	-0.00	-0.08		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1456	1igl		25	94	6.8e-25	0.37	1.00		GROWTH FACTOR INSULIN- LIKE GROWTH FACTOR II (IGF- II, IGF-2) 1IGL 3 (NMR, 20 STRUCTURES) 1IGL 4 1IGL 78	
1456	1igl		25	94	6.8e-25			108.25	GROWTH FACTOR INSULIN- LIKE GROWTH FACTOR II (IGF- II, IGF-2) 1IGL 3 (NMR, 20 STRUCTURES) 1IGL 4 1IGL 78	
1456	3lri	A	16	93	4.5e-25	-0.15	1.00		INSULIN-LIKE GROWTH FACTOR I; CHAIN: A;	GROWTH FACTOR INSULIN-LIKE GROWTH FACTOR-I, GROWTH FACTOR, NMR, PROTEIN 2 STRUCTURE, DISTANCE GEOMETRY
1458	2ocx	E	46	132	6.8e-37	0.33	1.00		CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J;	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									K, L, M, N, O, P, Q,	OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1458	2occ	E	46	132	6.8e-37			115.24	CYTOCHROME C OXIDASE; CHAIN: A, B, C, D, E, F, G, H, I, J, K, L, M, N, O, P, Q,	OXIDOREDUCTASE FERROCYTOCHROME C:OXYGEN OXIDOREDUCTASE; OXIDOREDUCTASE, CYTOCHROME(C)-OXYGEN, CYTOCHROME C 2 OXIDASE
1459	1avs	A	601	640	0.009	0.64	1.00		TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
1459	1awj		332	408	3e-11	0.01	0.29		ITK; CHAIN: NULL;	TRANSFERASE IL-2-INDUCIBLE T- CELL KINASE; TRANSFERASE, REGULATORY INTRAMOLECULAR COMPLEX, KINASE
1459	1b8q	A	248	365	1e-18	-0.14	0.87		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1459	1be9	A	248	341	3.4e-16	0.28	0.92		PSD-95; CHAIN: A; CRIFT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1459	1g2b	A	334	392	3e-12	-0.25	0.54		SPECTRIN ALPHA CHAIN; CHAIN: A;	METAL BINDING PROTEIN CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, SH3 2 DOMAIN, CYTOSKELETON
1459	1gbr	A	340	408	4.5e-11	-0.16	0.13		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED	

SEQ ID NO:	PDB ID	CHAI NID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1459	1gfc		349	408	1e-10	0.36	0.66		WITH SOS-A PEPTIDE IGBR 4 (NMR, 29 STRUCTURES) IGBR 5	
1459	1gky		479	663	1e-68			146.00	ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) IGC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) IGC 4 TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1 GKY 3 GUANOSINE MONOPHOSPHATE IGC 4	
1459	1gky		480	662	1e-68	0.80	1.00		TRANSFERASE GUANYLATE KINASE (E.C.2.7.4.8) COMPLEX WITH 1 GKY 3 GUANOSINE MONOPHOSPHATE IGC 4	
1459	1il6		253	345	1.1e-16	0.31	0.95		INTERLEUKIN 16; CHAIN: NULL;	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN
1459	1kwa	A	254	337	3e-17	0.19	1.00		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1459	1kwa	A	257	338	3.4e-16	0.07	0.98		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1459	1pdr		253	342	3.4e-14	0.19	0.96		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1459	1pwt		347	408	4.5e-11	0.46	0.58		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1459	1qau	A	254	362	1.5e-17	0.13	0.98		NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	OXIDOREDUCTASE BETA-FINGER
1459	1qav	A	250	336	4.5e-16	0.24	1.00		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER
1459	1qkw	A	350	408	3e-11	0.10	0.48		ALPHA II SPECTRIN; CHAIN: A;	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN
1459	1qly	A	349	408	1.3e-10	0.41	0.47		TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 2 SH3 DOMAIN
1459	1sem	A	350	408	1.5e-10	-0.10	0.41		SEM-5; 1 SEM 3 CHAIN: A, B; 1 SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1 SEM 8 CHAIN: C, D 1 SEM 10	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1 SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1 SEM 19
1459	1tud		334	392	6e-13	0.22	0.40		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT 2 SH3 DOMAIN, CYTOSKELETON
1459	1ukz		477	659	1.4e-07	0.10	0.69		TRANSFERASE URIDYLATE KINASE (E.C.2.7.4.-) COMPLEXED WITH ADP AND AMP 1UKZ 3.	
1459	1zak	A	482	662	1.2e-05	0.02	0.22		ADENYLATE KINASE; CHAIN:	TRANSFERASE ATP-AMP.

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									A, B;	PHOSPHOTRANSFERASE, TRANSFERASE
1459	3adk		475	662	9e-06	0.12	0.98		TRANSFERASE(PHOSPHOTRANSFERASE) ADENYLATE KINASE (B.C.2.7.4.3) 3ADK 4	
1459	3pdz	A	253	332	1.5e-13	0.32	1.00		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTPIE, PTP-BAS, SPECIFICITY 2 OF BINDING
1459	3tmk	C	479	662	9e-10	0.28	0.04		THYMIDYLATE KINASE; CHAIN: A, B, C, D, E, F, G, H;	KINASE KINASE, PHOSPHOTRANSFERASE
1459	4tmk	A	478	662	7.5e-16	-0.03	0.19		THYMIDYLATE KINASE; CHAIN: A;	TRANSFERASE ATP-DTMP PHOSPHOTRANSFERASE
1461	1bg3	A	1	498	0	1.13	1.00		HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
1461	1bg3	A	1	499	0			459.01	HEXOKINASE; CHAIN: A, B;	HEXOKINASE ATP/D-HEXOSE-6-PHOSPHOTRANSFERASE; HEXOKINASE, PHOSPHOTRANSFERASE
1461	1cza	N	1	501	0	1.07	1.00		HEXOKINASE TYPE I; CHAIN: N;	TRANSFERASE STRUCTURALLY HOMOLOGOUS DOMAINS
1464	1a0j	A	30	239	1.4e-80	0.88	1.00		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0j	A	30	239	1.4e-80			104.84	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1464	1a0l	A	30	233	1.7e-74	0.50	1.00		BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1464	1a0l	A	30	239	1.7e-74			97.00	BETA-TRYPTASE; CHAIN: A, B,	SERINE PROTEINASE TRYPSIN-LIKE

SEQ ID NO:	PDB ID	CHAI N ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									C, D;	SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1464	1bru	P	30	239	1.7e-75	0.64	1.00		ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1464	1bru	P	30	239	1.7e-75			115.93	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1464	1qpo		30	239	1.7e-79			98.94	TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, ZYMOGEN, 2 SIGNAL, MULTIGENE FAMILY
1464	1fuj	A	30	237	6e-71			200.42	PR3; CHAIN: A, B, C, D;	HYDROLASE (SERINE PROTEASE) MYELOBLASTIN; HYDROLASE, SERINE PROTEASE, GLYCOPROTEIN, ZYMOGEN, SIGNAL
1464	1mct	A	30	239	8.5e-83	0.74	1.00		COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	
1464	1mct	A	30	239	8.5e-83			103.86	COMPLEX(PROTEINASE/INHIBITOR) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH INHIBITOR FROM BITTER IMCT 3 GOURD IMCT 4	
1464	1ppf	E	30	237	1e-65			315.52	HYDROLASE(SERINE PROTEINASE) HUMAN LEUKOCYTE ELASTASE (HLE) (NEUTROPHIL ELASTASE (HNE)) IPPF 3 (E.C.3.4.21.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY IPPF 4 OVOMUCOID INHIBITOR (OMTKY3) IPPF 5	